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In re Patent Application of:  
Timothy A. Coleman

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Group Art Unit: 1653

Filed: August 3, 2001

Examiner: Not Yet Assigned

For: Vascular Endothelial Growth Factor 2

**SUBMISSION OF REPLACEMENT/SUBSTITUTE DRAWINGS**

Attn: Draftsperson  
Commissioner for Patents  
Washington, DC 20231

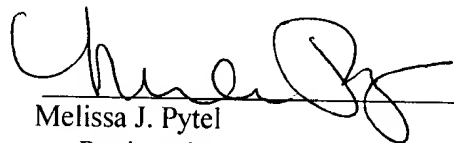
Sir:

Applicants submit herewith replacement/substitute Figures 1A-31U (68 sheets) to replace Figures 1A-31G (47 sheets) as originally filed. Additional pages are due to reorganization of the drawings in order to comply with the margin requirements under 37 C.F.R. § 1.84. No new matter is introduced.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: April 17, 2003

  
\_\_\_\_\_  
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1  
GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTCTGCTCGCCGCTG  
-----+-----+-----+-----+-----+-----+-----+  
CAGGAAGGTGGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAAGACGAGCGGGGAC  
M H S L G F F S V A C S L L A A A  
60

61  
CGCTGCTCCCGGGTCTCGCGAGGCGCCCGCCCGCCCGCCCGCTTCGAGTCCGGACTCG  
-----+-----+-----+-----+-----+-----+-----+  
GCGACGAGGGCCAGGAGCGCTCCGGGGCGGGCGGGCGGGAAGCTCAGGCCCTGAGC  
L L P G P R E A P A A A A A F E S G L D  
120

121  
ACCTCTCGGACGGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAGATCTGG  
-----+-----+-----+-----+-----+-----+-----+  
TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCTGTTCTAGACC  
L S D A E P D A G E A T A Y A S K D L E  
180

181  
AGGAGCAGTTACGGTCTGTGTCCAGTGTAGATGAACCTCATGACTGTACTCTACCCAGAAT  
-----+-----+-----+-----+-----+-----+-----+  
TCCTCGTCAATGCCAGACACAGGTCAACATCTACTTGAGTACTGACATGAGATGGGTCTTA  
E Q L R S V S S V D E L M T V L Y P E Y  
240

241  
ATTGGAAAATGTACAAGTGTCAAGCTAAGGAAAGAGGCTGGCAACATAACAGAGAACAGG  
-----+-----+-----+-----+-----+-----+-----+  
TAACCTTTTACATGTTACAGTCGATTCCCTTTCCCTCCGACCGTTGTATTGTCTCTTGTCC  
W K M Y K C Q L R K G G W Q H N R E Q A  
300

301  
CCAACCTCAACTCAAGACAGAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG  
-----+-----+-----+-----+-----+-----+-----+  
GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTAAACGACGTCGTGTAATATATGTC  
N L N S R T E E T I K F A A A H Y N T E  
360

FIG. 1A

MATCH WITH FIG. 1B



**MATCH WITH FIG. 1B**

661		720
TTTACAGACAAGTTTCATTCCTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	
AAATGTCTGTTTCAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACAG		
Y R Q V H S I I R R S L P A T L P Q C Q		
721		780
AGGCAGCGAACAAGACCTGCCCCCACCCAATTACATGTGGAATAATCACATCTGCAGATGCC	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	
TCCGTCGCTTGTCTGGACGGGTGGTTAATGTACACCTTATTAGTGTAGACGCTACGG		
A A N K T C P T N Y M W N N H I C R C L		
781		840
TGGCTCAGGAAGATTTTATGTTTTCCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	
ACCGAGTCCCTTCTAAAAATACAAAAGGAGCCCTACGACCCTCTACTGAGTTGTCTACCTAAGG		
A Q E D F M F S S D A G D D S T D G F H		
841		900
ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCCTGTCAGTGTCTGCAGAG	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	
TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC		
D I C G P N K E L D E E T C Q C V C R A		
901		960
CGGGGCTTCGGCCTGCCAGCTGTGGACCCCCACAAGAAGAACTAGACAGAAACTCATGCCCAGT	- - - - - + - - - - - + - - - - - + - - - - - + - - - - - +	
GCCCCGAAGCCGGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA		
G L R P A S C G P H K E L D R N S C Q C		

**FIG. 1C**

**MATCH WITH FIG. 1D**

MATCH WITH FIG. 1C

961	GTGTCGTGTAACAACTCTTCCCCAGCCCAATGTGGGGCCAAACCGAGAAATTTGATGAAA -----+-----+-----+-----+-----+-----+-----+ CACAGACATTTTGTGAGAAAGGGTCCGGTTACACCCCGGTGGCTCTTAAACTACTTT V C K N K L F P S Q C G A N R E F D E N	1020
1021	ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA -----+-----+-----+-----+-----+-----+-----+ TGTGTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGATTTAGGACCTT T C Q C V C K R T C P R N Q P L N P G K	1080
1081	AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAAGGAAAGATTCC -----+-----+-----+-----+-----+-----+-----+ TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTCCCTTCTCAAGG C A C E C T E S P Q K C L L K G K K F H	1140
1141	ACCACCAAACATGCAGCTGTTACAGACGGCCCATGTACGAACCCGCCAGAGGCTGTGAGC -----+-----+-----+-----+-----+-----+-----+ TGGTGGTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAAACACTCG H Q T C S C Y R R P C T N R Q K A C E P	1200
1201	CAGGATTTTCATATAGTGAAGAAGTGTGTGCTTGTGTCCCTTCATATTTGGCAAAGACCAC -----+-----+-----+-----+-----+-----+-----+ GTCCTAAAAGTATATCACTTCTTACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG G F S Y S E E V C R C V P S Y W Q R P Q	1260

FIG. 1D

MATCH WITH FIG. 1E

MATCH WITH FIG. 1D

1261	AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTCTATATGGAACCTGTGT -----+-----+-----+-----+-----+-----+-----+ TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA	1320
	M S *	
1321	TGCCACAGTAGAACTGTCTGTGAACAGAGAGAGACCCCTTGTGGGTCCATGCTAACAAAGACA -----+-----+-----+-----+-----+-----+-----+ ACGGTGTCACTTTGACAGACACTTGTCTCTCTGGAACACCCAGGTACGATTGTTTCTGT	1380
1381	AAAGTCTGTCTTTCCCTGAACCATGTGGATAACTTTACAGAAAATGGACTGGAGCTCATCTG -----+-----+-----+-----+-----+-----+-----+ TTTCAGACAGAAAAGGACTTGGTACACCTATTGAAAATGCTTTACCTGACCTCGAGTAGAC	1440
1441	CAAAAGGCCCTCTGTAAAGACTGGTTTTCTGCCAATGACCAACAGCCAAGATTTCCCTC -----+-----+-----+-----+-----+-----+-----+ GTTTCCGGAGAACATTTCTGACCAAAAAGACGGTTACTGGTTTGTCTCGGTTCTAAAAGGAG	1500
1501	TTGTGATTTCTTTAAAGAAATGACTATATAATTTATTTCCACTAAAAATATGTTTCTGTC -----+-----+-----+-----+-----+-----+-----+ AACACTAAAGAAATTTCTTACTGATATATTAATAAAGGTGATTTTATAACAAAGACG	1560
1561	ATTCAATTTTATAGCAACAACAATTTGGTAAAACTCACTGTGATCAATAATTTTATATCAT -----+-----+-----+-----+-----+-----+-----+ TAAGTAAAAATATCGTTGTTGTTAACCATTTTGTAGTGACACTAGTTATAAAAAATATAGTA	1620
1621	GCAAAAATATGTTTAAAAATAAAATGAAAAATTGTATTTATATAAAAAA -----+-----+-----+-----+-----+-----+-----+ CGTTTTATACAAAATTTTATTTTACTTTTAAACATAAAATATTTTATTTT	1674

FIG. 1E

```

1      CGAGGCCACGGCTTATGCAAGCAAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
      -----+-----+-----+-----+-----+-----+-----+
      .      .      .      .      .      .      .      .      .      .
61     AGATGAACTCATGACTGTACTCTACCCAGAATAATTGGAATAATGTACAAGTGTCAAGCTAAG
      -----+-----+-----+-----+-----+-----+-----+
      M T V L Y P E Y W K M Y K C Q L R
      .      .      .      .      .      .      .      .      .      .
121    GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
      -----+-----+-----+-----+-----+-----+-----+
      K G G W Q H N R E Q A N L N S R T E E T
      .      .      .      .      .      .      .      .      .      .
181    TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
      -----+-----+-----+-----+-----+-----+-----+
      I K F A A A H Y N T E I L K S I D N E W
      .      .      .      .      .      .      .      .      .      .
241    GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGAAGGAGTTTGAGT
      -----+-----+-----+-----+-----+-----+-----+
      R K T Q C M P R E V C I D V G K E F G V
      .      .      .      .      .      .      .      .      .      .
301    CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGTTGCTG
      -----+-----+-----+-----+-----+-----+-----+
      A T N T F F K P P C V S V Y R C G G C C
  
```

FIG. 2A

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

421 TGAAATTACAGTGCCCTCTCTCTCAAGGCCCCCAACCAGTAACAATCAGTTTGGCCAATCA  
-----+-----+-----+-----+-----+  
E I T V P L S Q G P K P V T I S F A N H

481 CACTTCCTGCCGATGTCATAAAGTGGATGTTTACAGACAAGTTCATTCCATTATTAG  
-----+-----+-----+-----+-----+  
T S C R C M S K L D V Y R Q V H S I I R

541 ACGTTCCCTGCCAGCAACACTACACAGTGTTCAGGCAGCGAACAAGACCTGCCCCCAACAA  
-----+-----+-----+-----+-----+  
R S L P A T L P Q C Q A A N K T C P T N

601 TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTTATGTTTTCCTC  
-----+-----+-----+-----+-----+  
Y M W N N H I C R C L A Q E D F M F S S

661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGGAGCT  
-----+-----+-----+-----+-----+  
D A G D D S T D G F H D I C G P N K E L

721 GGATGAAGAGACCTGTGAGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC  
-----+-----+-----+-----+-----+  
D E E T C Q C V C R A G L R P A S C G P

FIG. 2B

MATCH WITH FIG. 2C



MATCH WITH FIG. 2B

781 CCACAAAGAACTAGACAGAACTCATGCCAGTGTGTCTGTAAAAACAACCTCTTCCCCAG  
 -----+-----+-----+-----+-----+  
 H K E L D R N S C Q C V C K N K L F P S

841 CCAATGTGGGGCCACCGAGAAATTGATGAAAAACACATGCCAGTGTGTATGTAAAAAGAAC  
 -----+-----+-----+-----+-----+  
 Q C G A N R E F D E N T C Q C V C K R T

901 CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCCTGTGAATGTACAGAAAGTCC  
 -----+-----+-----+-----+-----+  
 C P R N Q P L N P G K C A C E C T E S P

961 ACAGAAATGCTTGTAAAAAGGAAAGAGTTCCACCACCAACATGCAGCTGTACAGACG  
 -----+-----+-----+-----+-----+  
 Q K C L L K G K K F H H Q T C S C Y R R

1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG  
 -----+-----+-----+-----+-----+  
 P C T N R Q K A C E P G F S Y S E V C

1081 TCGTGTGTCCCTTCATATTGGCAAAAGACCACAAATGAGCTAAGATTGTACTGTTTCCA  
 -----+-----+-----+-----+-----+  
 R C V P S Y W Q R P Q M S \*

FIG. 2C

MATCH WITH FIG. 2D

MATCH WITH FIG. 2C

1141 GTTCATCGATTTTCTATTATGGA AAACTGTGTGCCACAGTAGAACTGTCTGTGAACAGA  
-----+-----+-----+-----+-----+-----+-----+  
1201 GAGACCCCTTGTGGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCCCTGAACCATGTGGA  
-----+-----+-----+-----+-----+-----+-----+  
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGC AAAAGGCCCTCTTGTAAGACTGGTTTT  
-----+-----+-----+-----+-----+-----+-----+  
1321 CTGCCAATGACCAACAGCCCAAGATTTTCCCTCTTG TGATTTCTTTAAAGAAATGACTATA  
-----+-----+-----+-----+-----+-----+-----+  
1381 TAAATTTATTC CACTAAAAATATGTTTCTGCATTCATTTTATAGCAACAACAATGGT  
-----+-----+-----+-----+-----+-----+-----+  
1441 AAAACTCACTGTGATCAATATTTTATATCATGC AAAAATATGTTTAAAAATAAAATGAAAA  
-----+-----+-----+-----+-----+-----+-----+  
1501 TTGTATTATATAAAAAAAAAAAAAAA  
-----+-----+-----+-----+-----+-----+-----+

FIG. 2D

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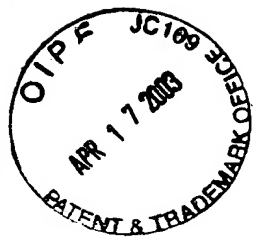
1 50  
Pdga .MRTLACLLL LCCYLALHL AEEAIPREV IERLARSQIH SIRDLORLLE  
Pdgb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLORLLH  
Vegf .....MNFL SWVHWSLALL LY..... .LHAKWSQA  
Vegf2 .....MTV LYPEYKMYK CQ..... .LRKGGWQH

51 100  
Pdga IDSVGSEDSL DTSRAHGVH ATKHVPEKRP LPIRRKRSI. ....EEAVP  
Pdgb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI  
Vegf APMAE.....GGCQ NHHEVVKFMD .VYQR.....  
Vegf2 REQANLNSRT EETIKFAAH YNTEILKSID NEWRK.....

101 150  
Pdga AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRC TGCC NTSSVKCQPS  
Pdgb AECKTRTEVF EISRRLLDRT NANFLVWPPC VEVQRC SGCC NNRNVCQRP  
Vegf SYCHPIETLV DIFQYDPI .EYIFKPS VPLMRCGGCC NDEGLEQVPT  
Vegf2 TOCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

151 200  
Pdga RVHHRSVKVA KVEYVRKKPK LKEVQRLEE HLEQAC..... AT.....  
Pdgb QVQLRPVQVR KIEIVRKKPI FKCATVTLED HLAQ..... ETVAARPVT  
Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCEQPKK DRARQEKKS  
Vegf2 STSYLSKTLF EIT.VPLSOG PKPVTISFAN HTSCROMSKL DVYRQVHSII

FIG. 3A



201 250  
Pdgha ..... TSLNPD YREEDIDVR.  
Pdghb RSPGGSQEQR AKTPQTRVTI RTVRVRRPPK GKHRKFKHTH DKTALKETLG  
Vegf RCK..... GKQKRRK KSRYSWSVY VGARCCMPW SLPQPHF  
Vegf2 RRSLPATLPQ COAANKTCPT NYMNNHICR CLAQEDFMFS SDAGDDSDTG

251 300  
Pdgha .....  
Pdghb A.....  
Vegf ..... CGP..... CSE RRKHLFVQDP QTCKCCKNT  
Vegf2 FHDICGNKE LDEETCCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

301 350  
Pdgha .....  
Pdghb .....  
Vegf ..... DSRCKARQ LELNERTCRC DKPRR.....  
Vegf2 LFPSQCCANR EFDENTCCQ VCKRTCPRNQ PLNPKKACE CTESPOKCLL

351 398  
Pdgha .....  
Pdghb .....  
Vegf .....  
Vegf2 KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCPVS YWQRPQMS

FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN  
 EACH PAIR OF GENES IS SHOWN IN THE  
 FOLLOWING TABLE

	PDGF $\alpha$	PDGF $\beta$	VEGF	VEGF-2
PDGF $\alpha$				
PDGF $\beta$	48.0			
VEGF	20.7	22.7		
VEGF-2	23.5	22.4	30.0	

FIG. 4

### Expression of VEGF2 mRNA in Human Breast Tumor Cells



Lane 1. normal breast tissue  
Lane 2. breast tumor tissue  
Lane 3-9. breast tumor cell lines.

**FIG. 5**

## Expression of VEGF-2 mRNA in Human Adult Tissues

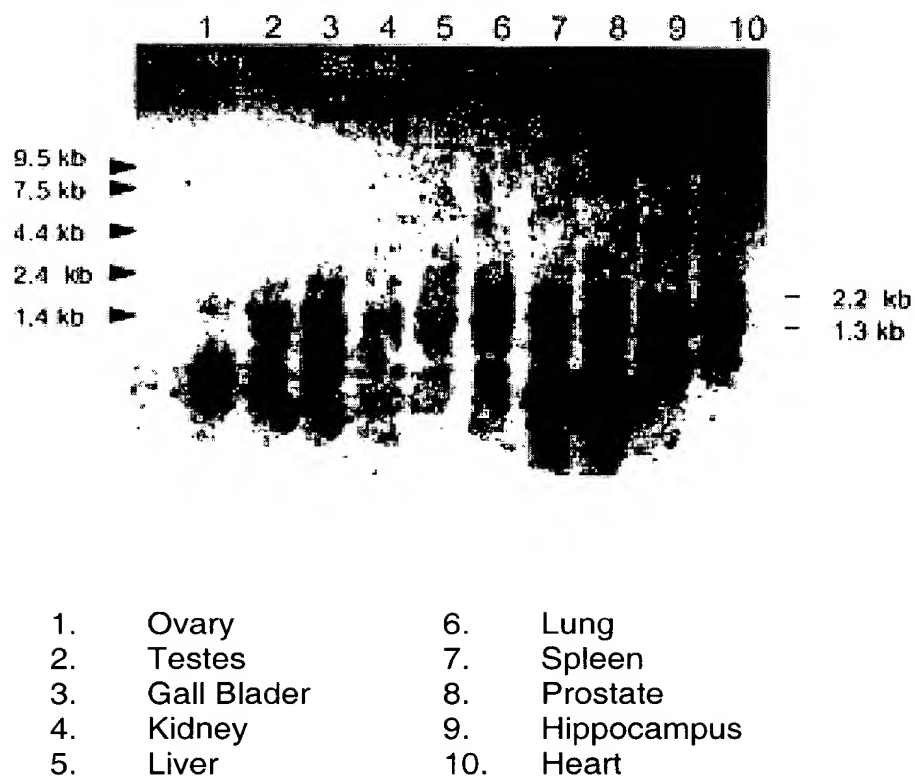
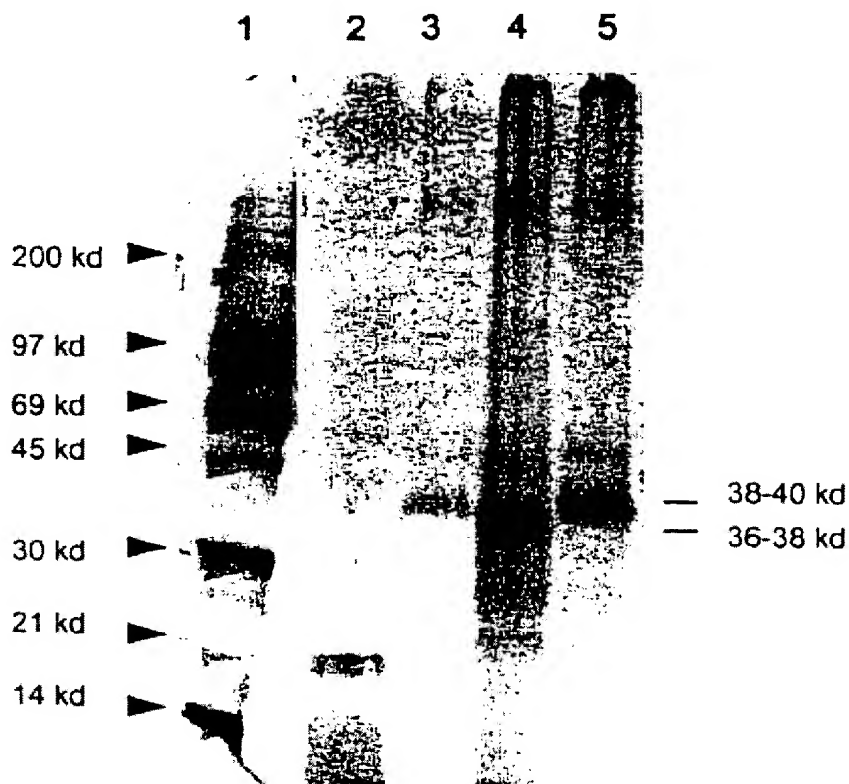


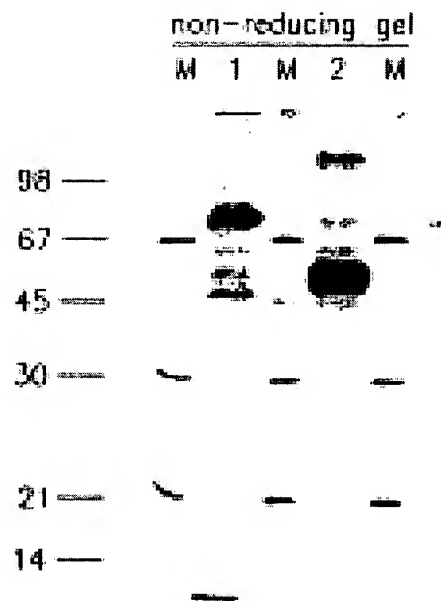
FIG. 6



Lane 1: 14-C and rainbow M.W. marker  
Lane 2: FGF control  
Lane 3: VEGF2 (M13-reverse & forward primer)  
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primer)  
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primer)

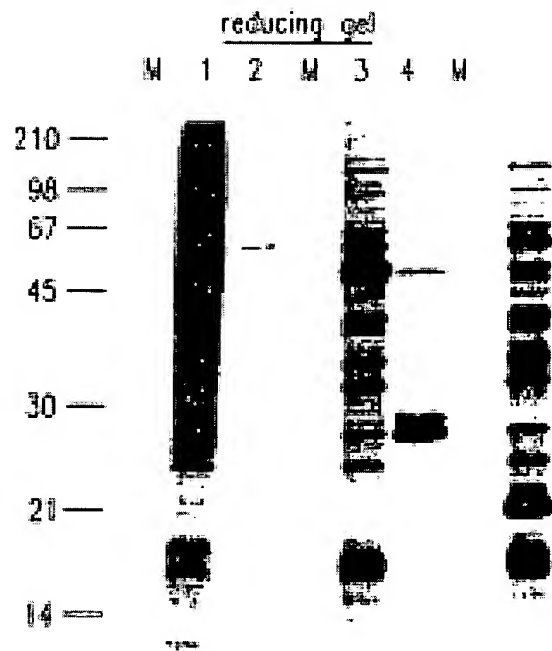
FIG. 7





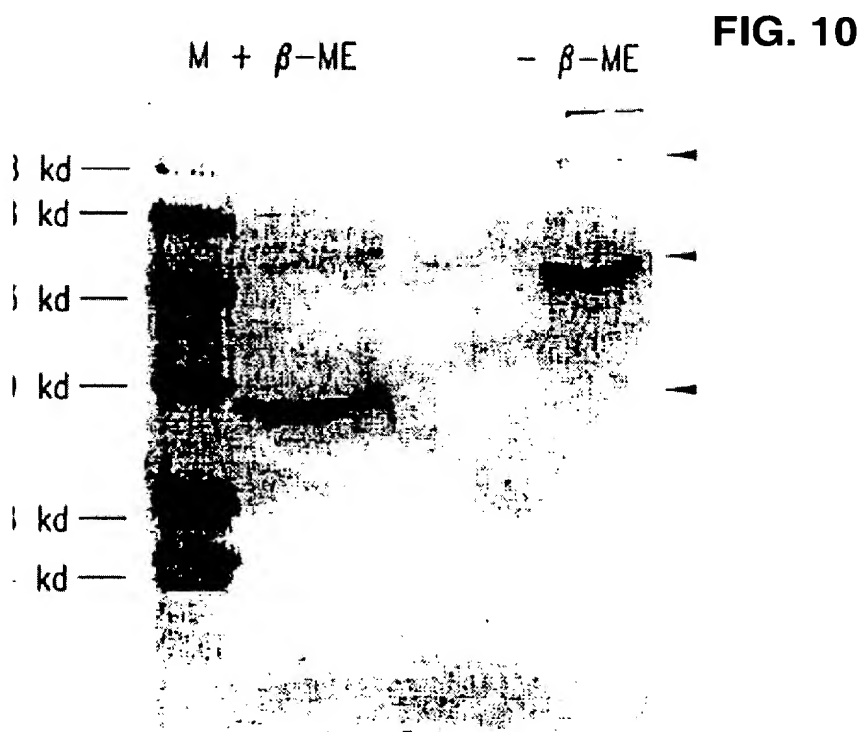
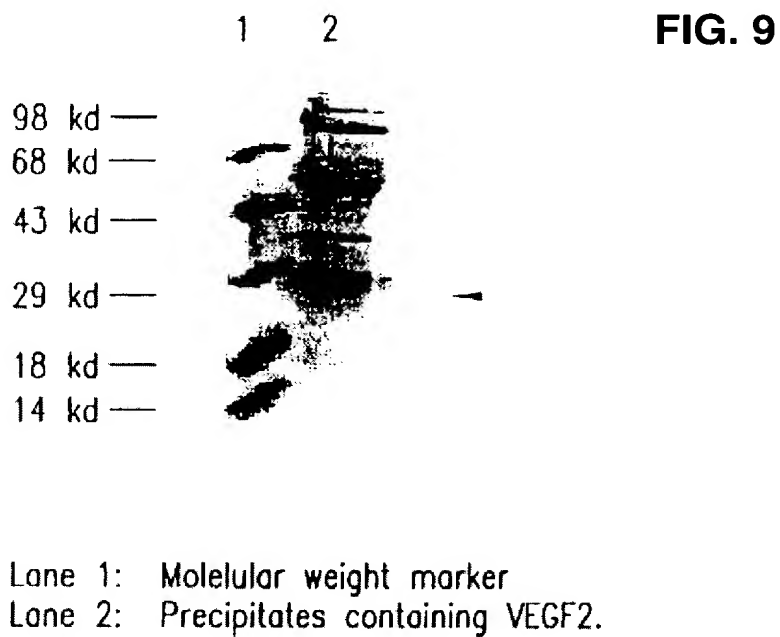
Lane M: Marker  
Lane 1: Vector medium  
Lane 2: VEGF2 medium

FIG. 8A



Lane M: Marker  
Lane 1: vector cytoplasm  
Lane 2: vector medium  
Lane 3: VEGF2 cytoplasm  
Lane 4: VEGF2 medium

FIG. 8B



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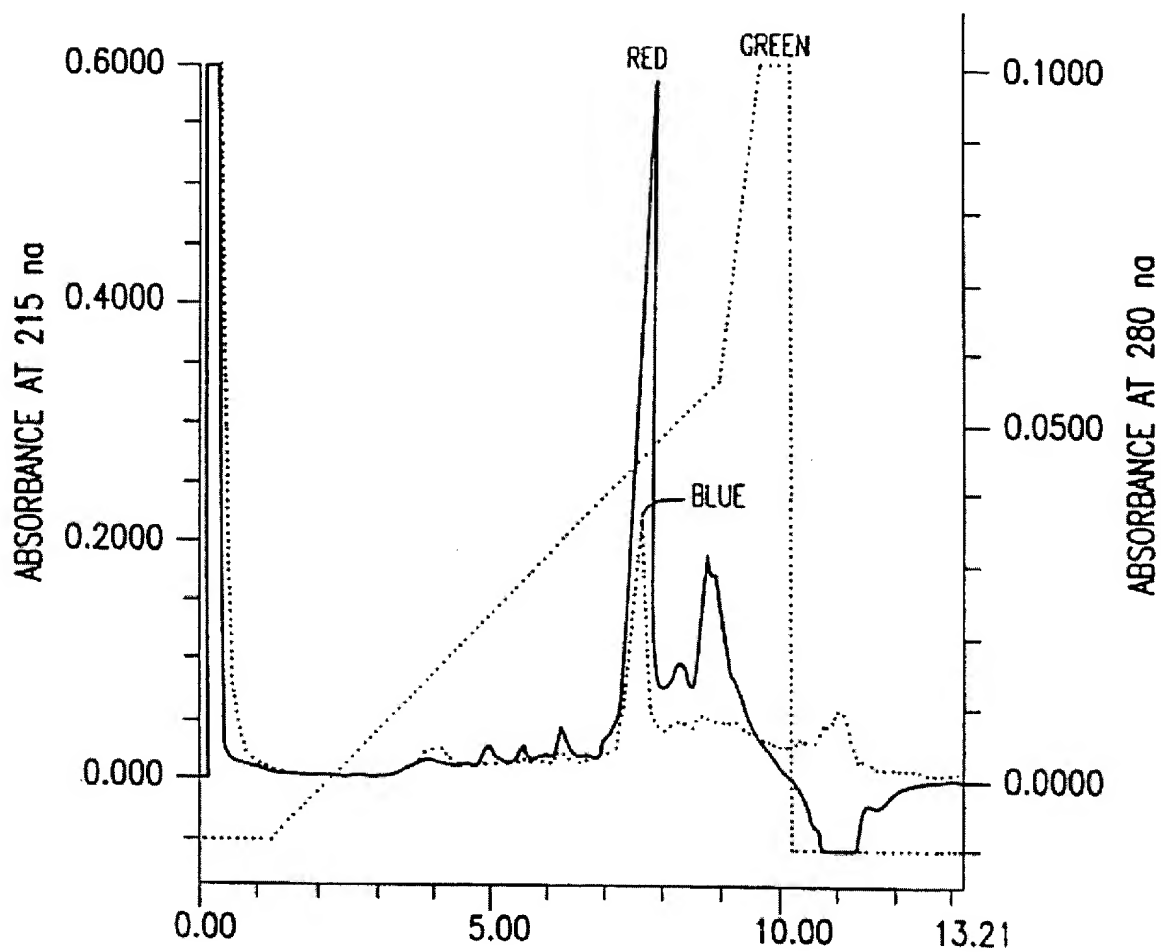


FIG. 11

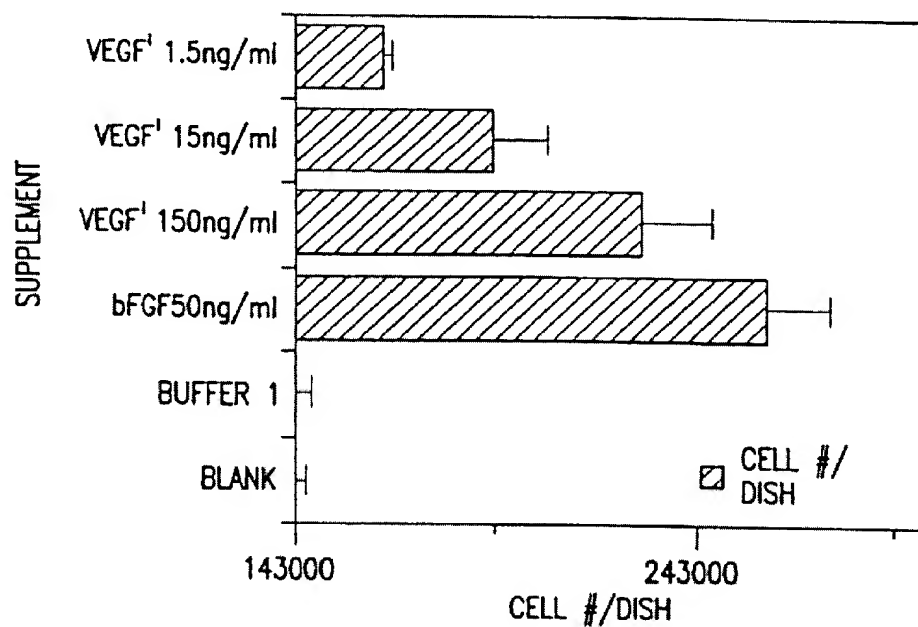


FIG. 12

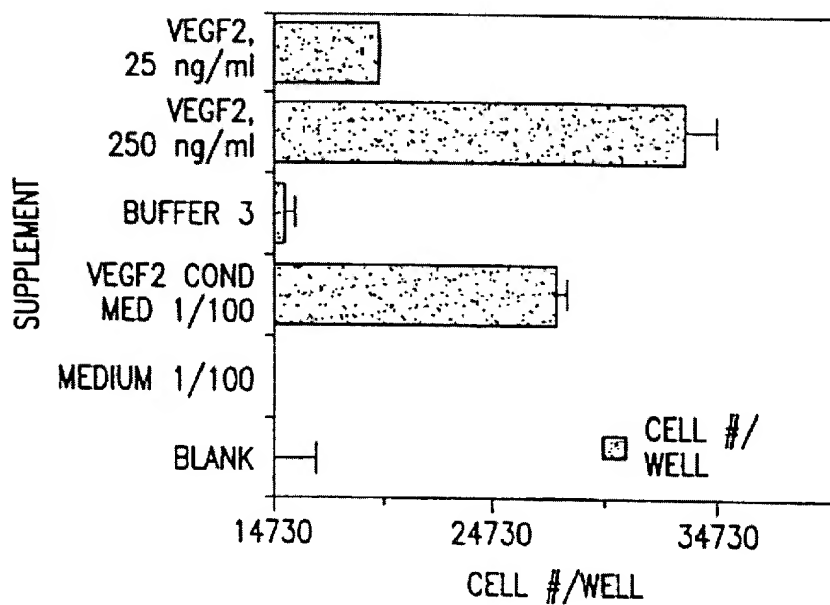


FIG. 13

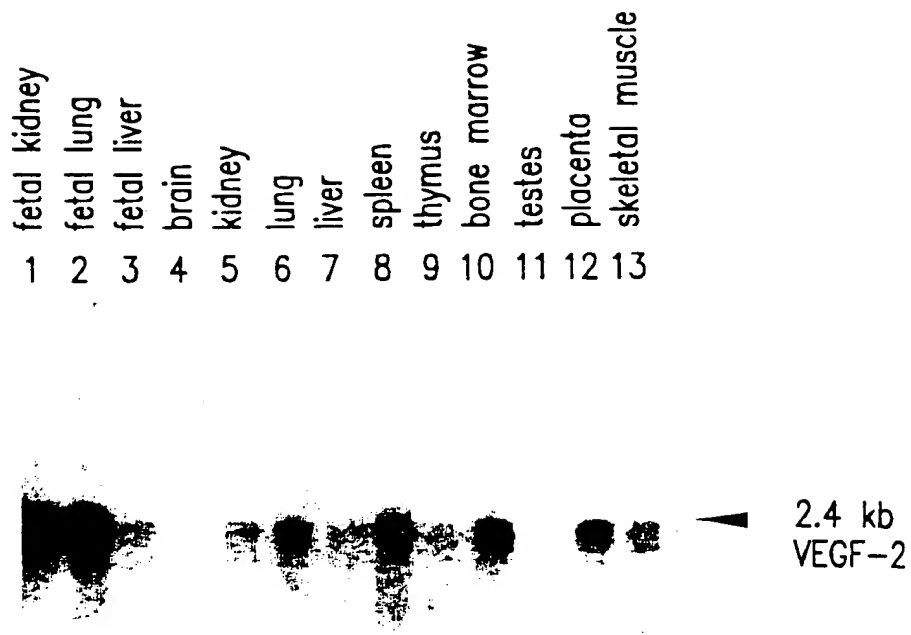


FIG. 14A

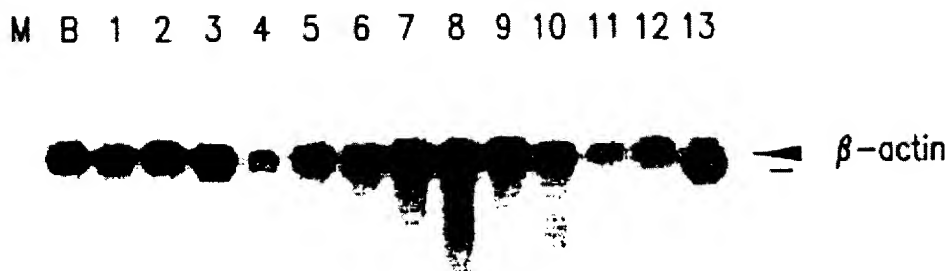


FIG. 14B

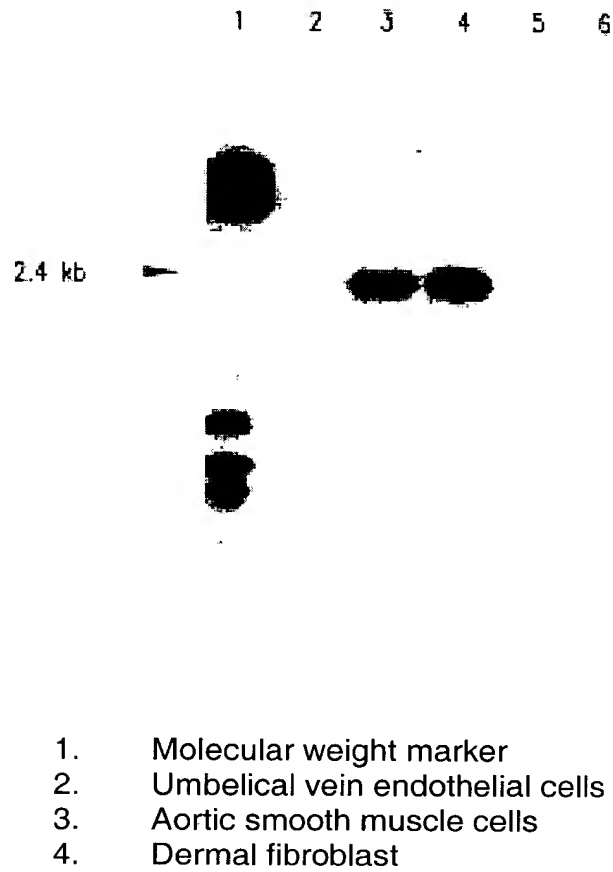
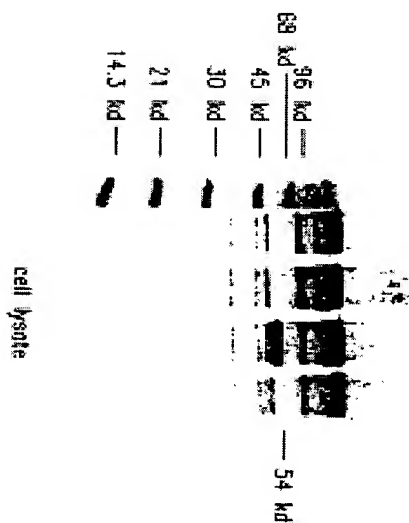


FIG. 15



1. Molecular weight marker
2. Blank
3. Control protein-HA
4. Vector control
5. VEGF2-HA

FIG. 16A



1. Molecular weight marker
2. Blank
3. Control protein-HA
4. VEGF2-HA
5. Vector control

FIG. 16B



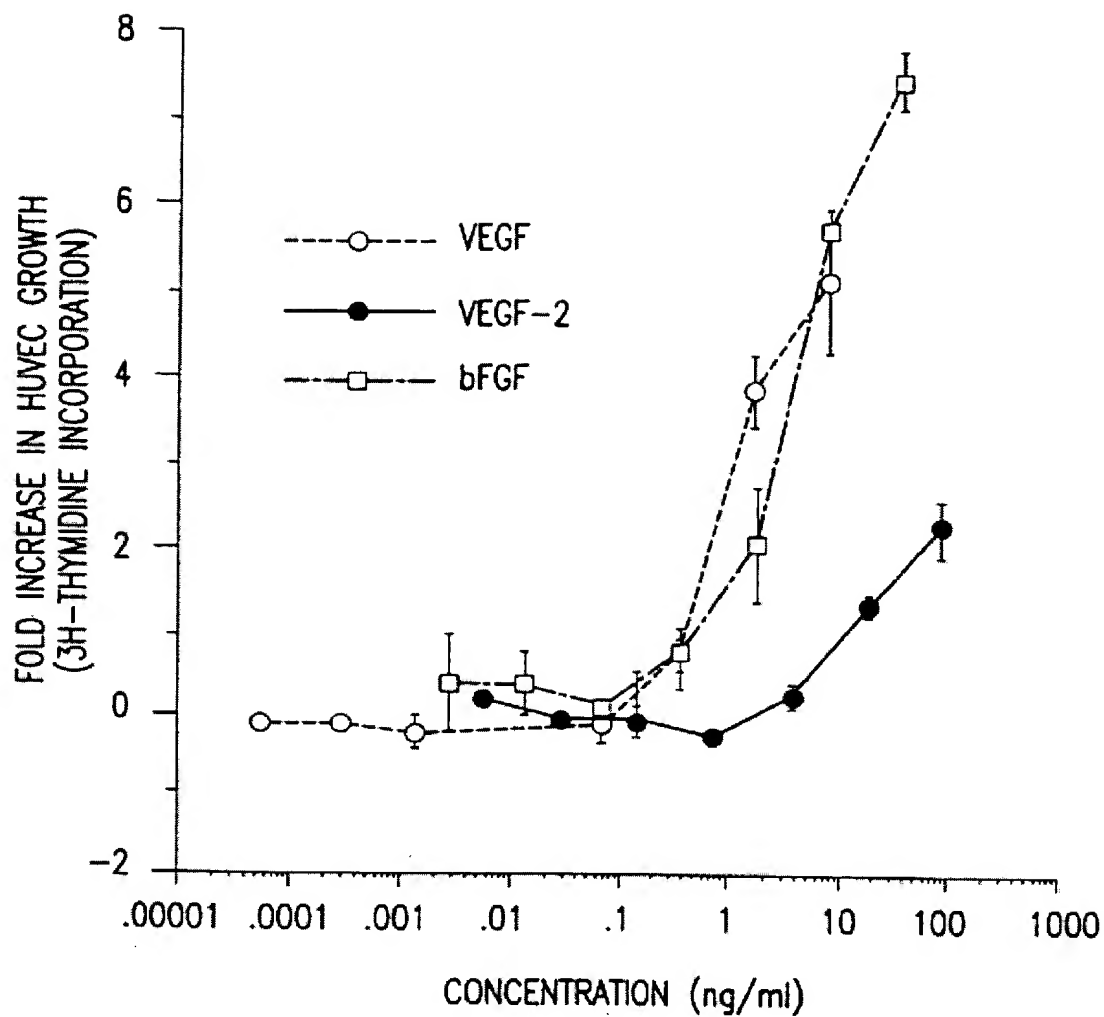


FIG. 17

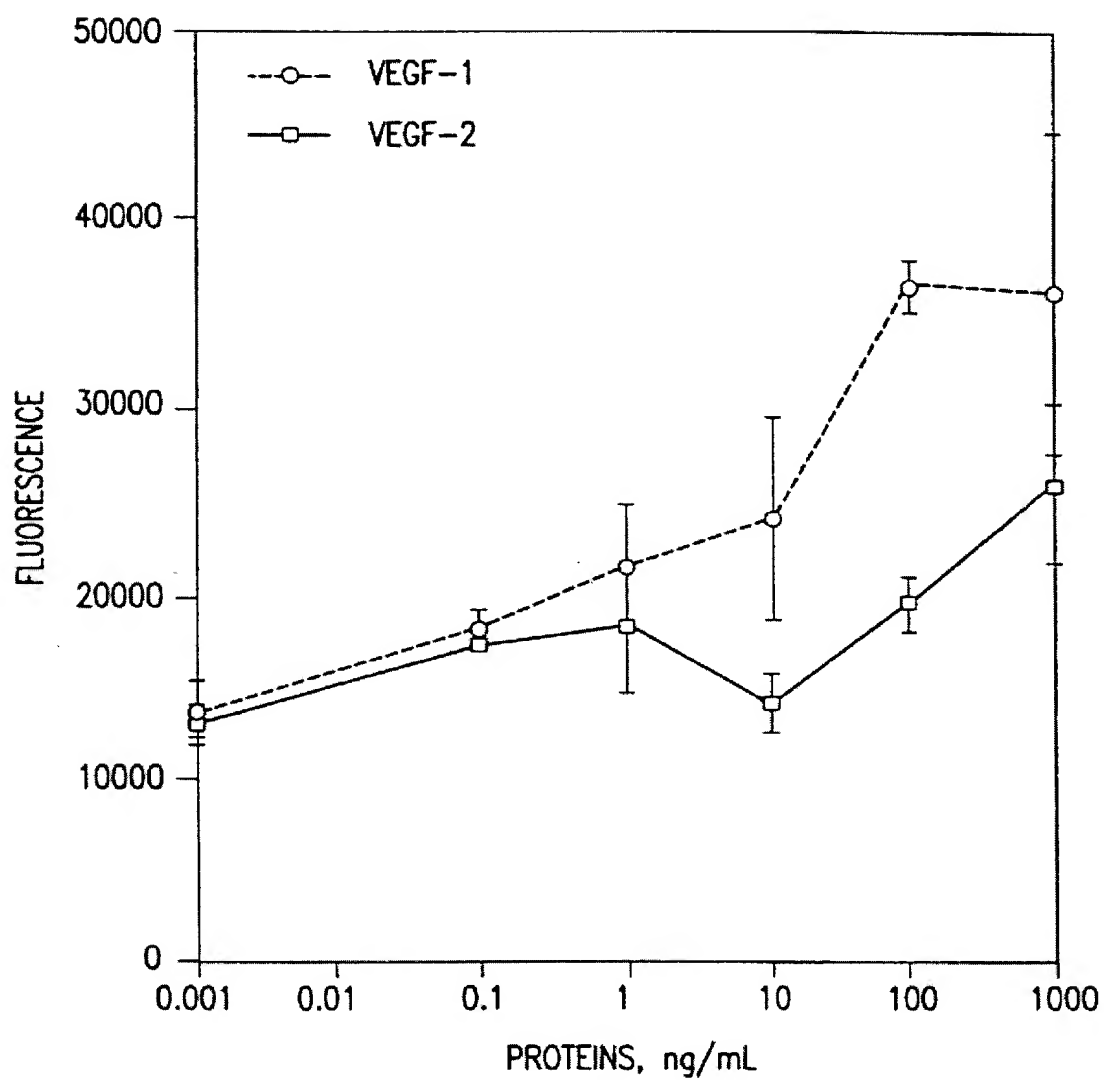


FIG. 18

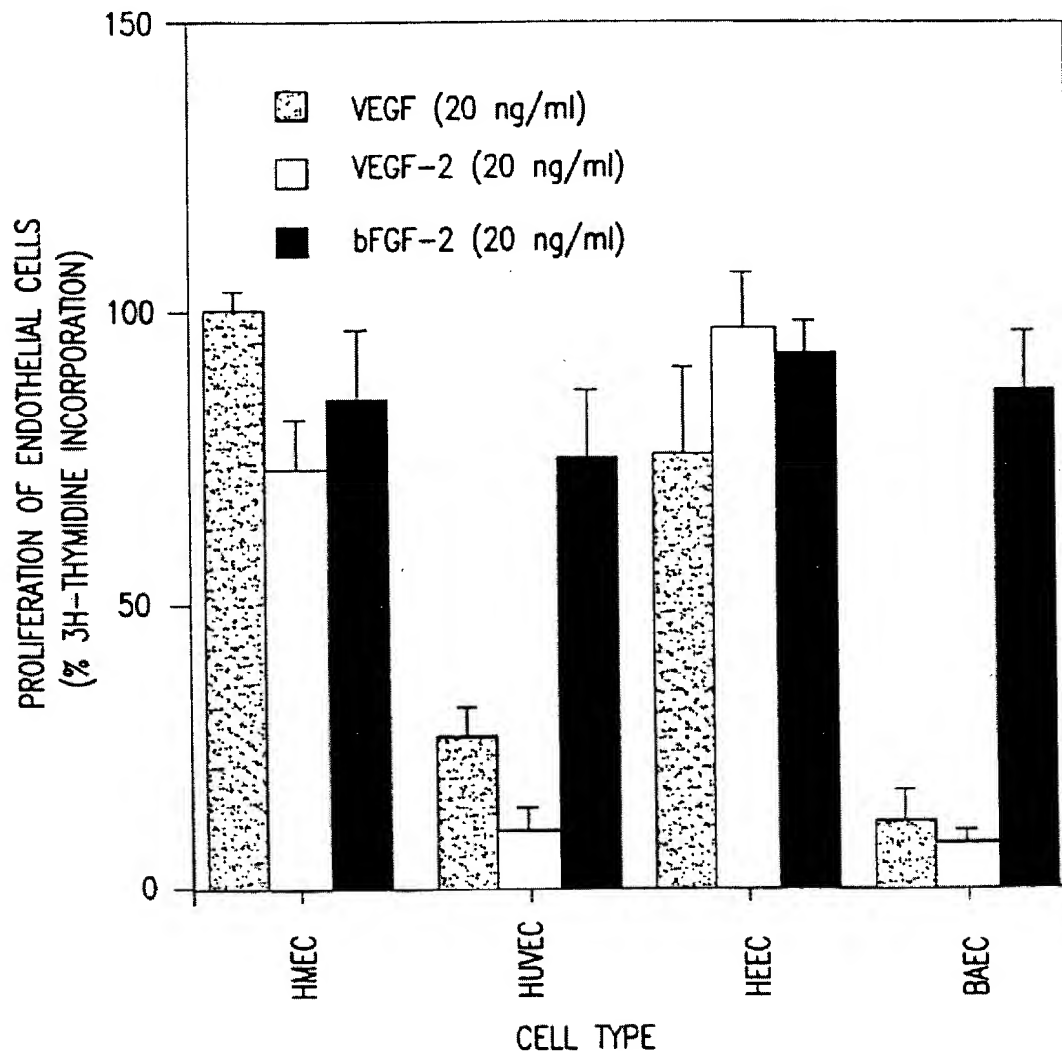


FIG. 19

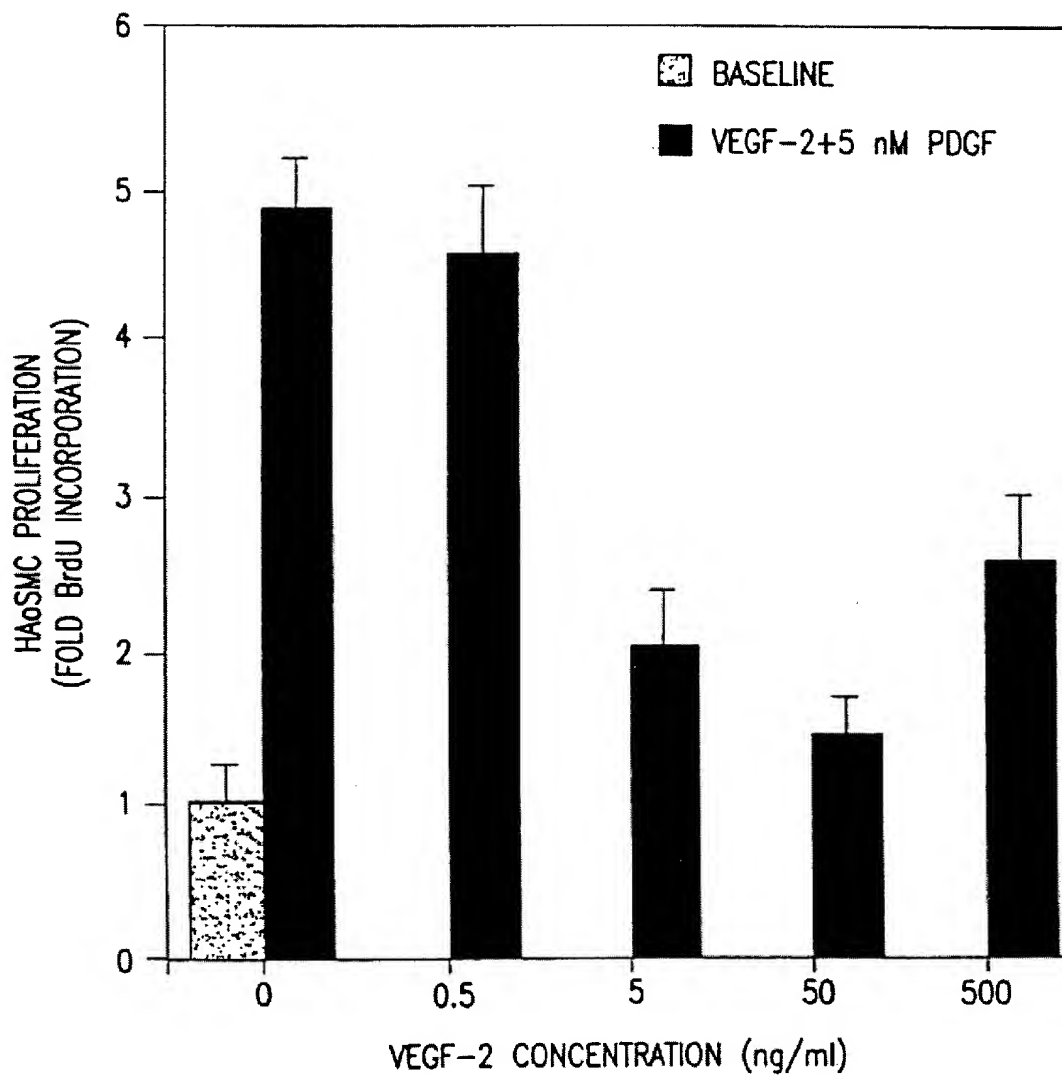


FIG. 20A

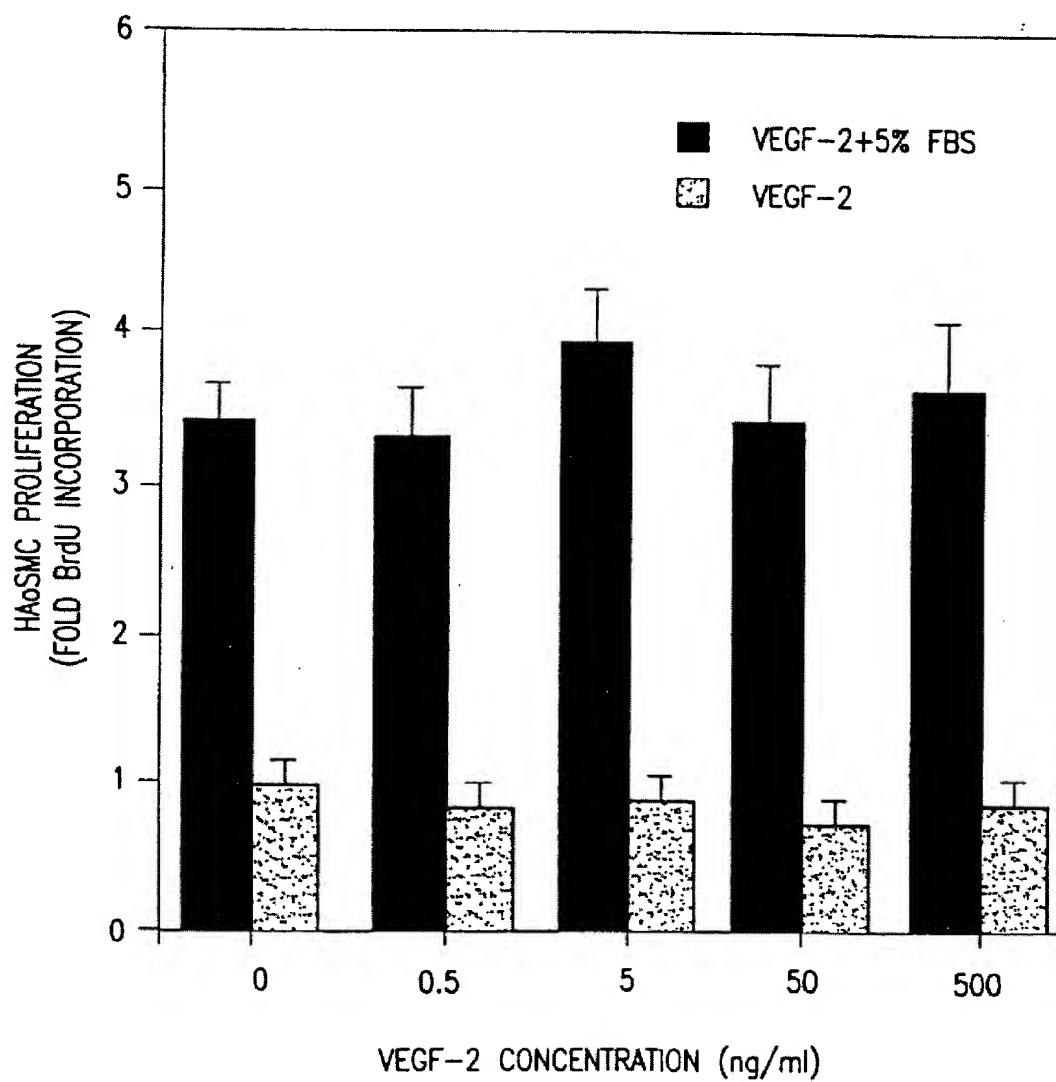


FIG. 20B

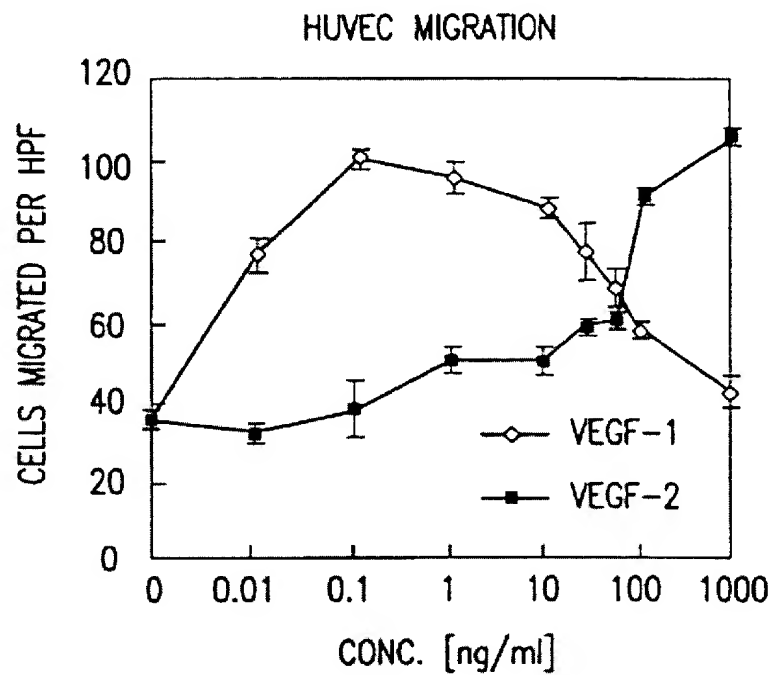


FIG. 21A

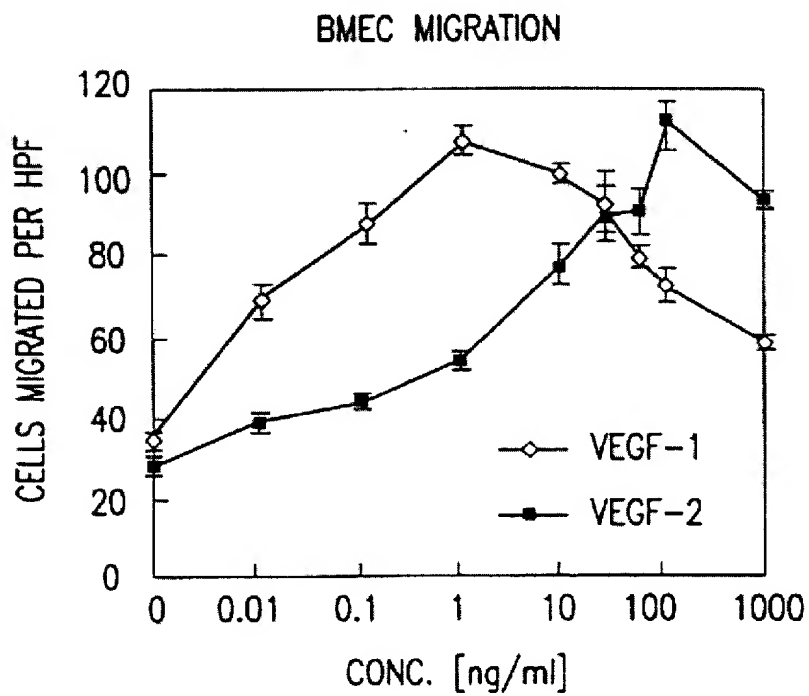


FIG. 21B

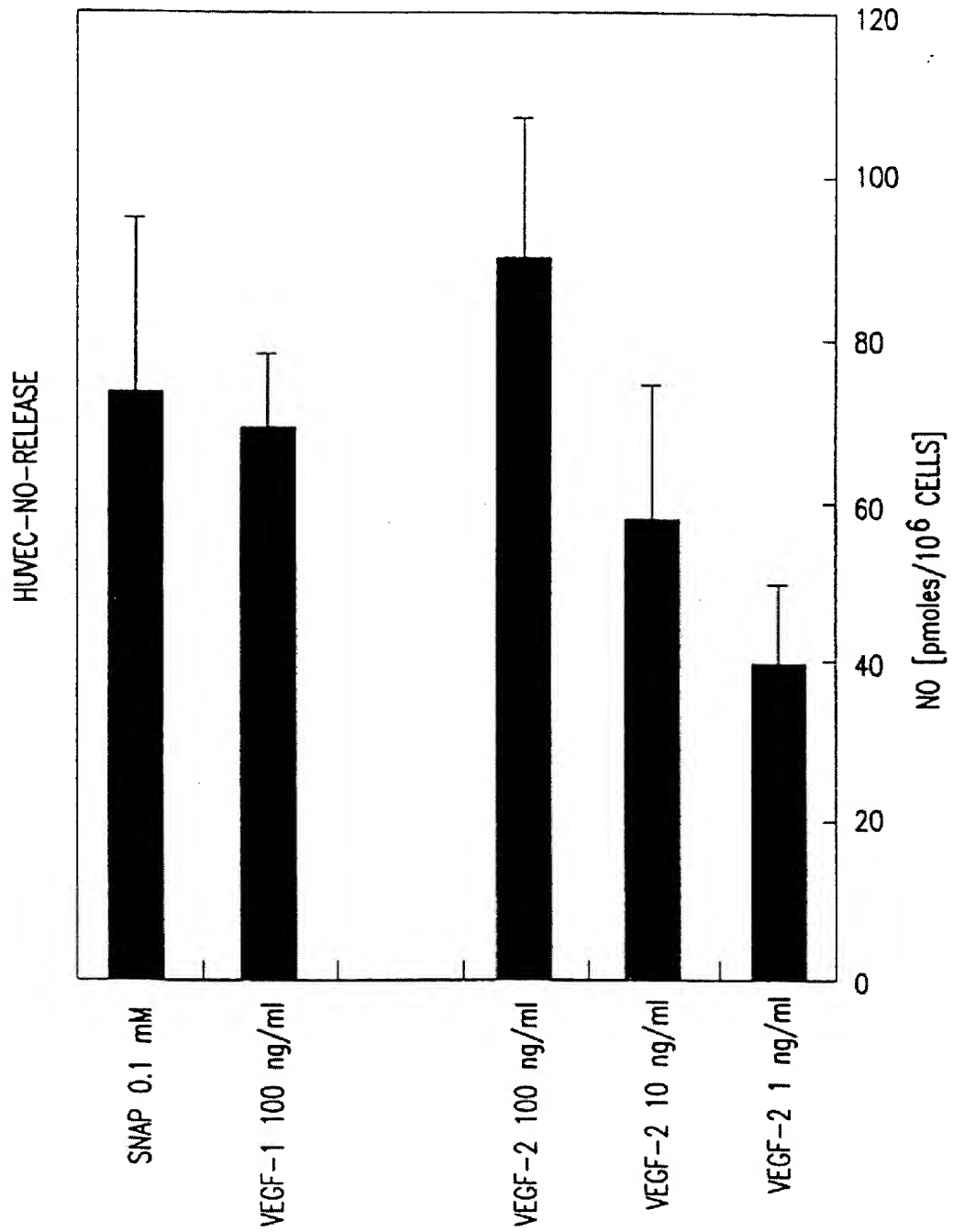


FIG. 22

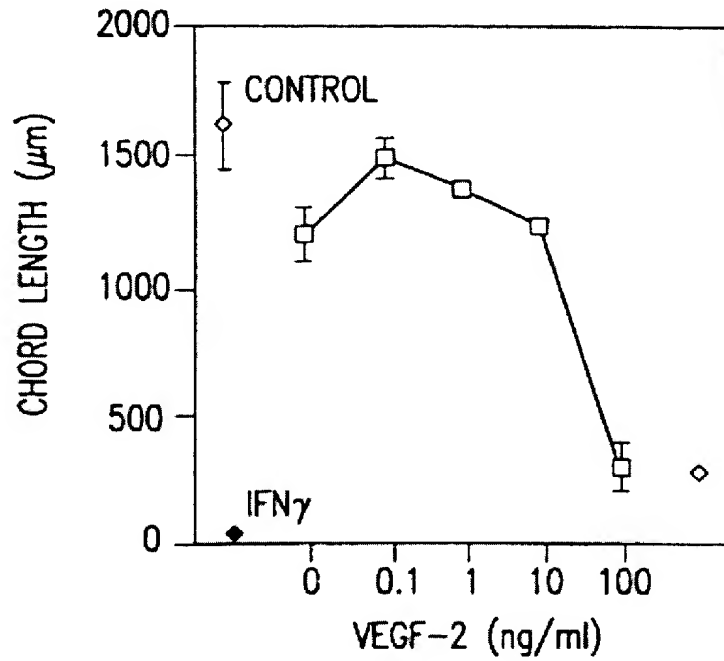


FIG. 23

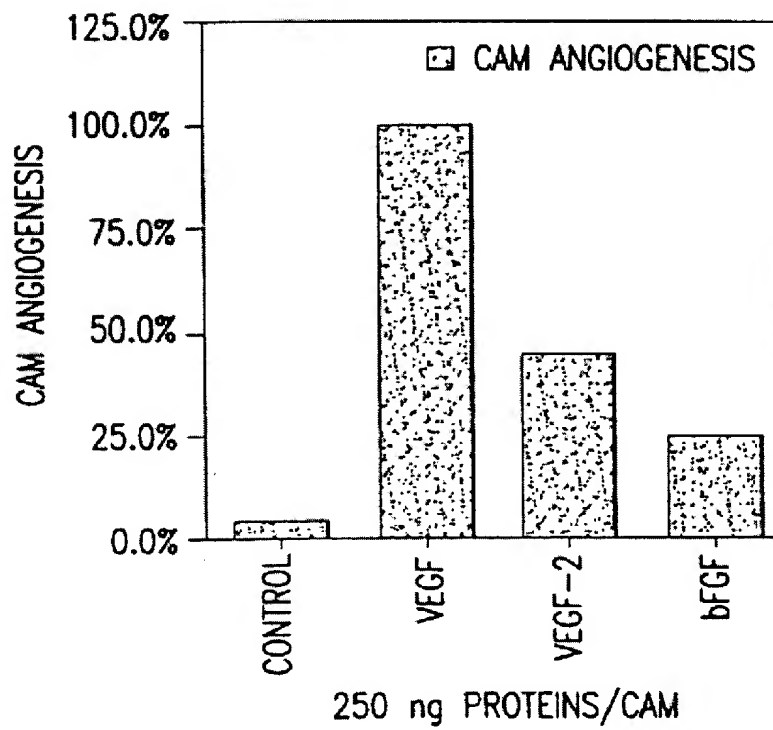


FIG. 24



CALF BLOOD PRESSURE RATIO  
-PROTEIN I.A.-

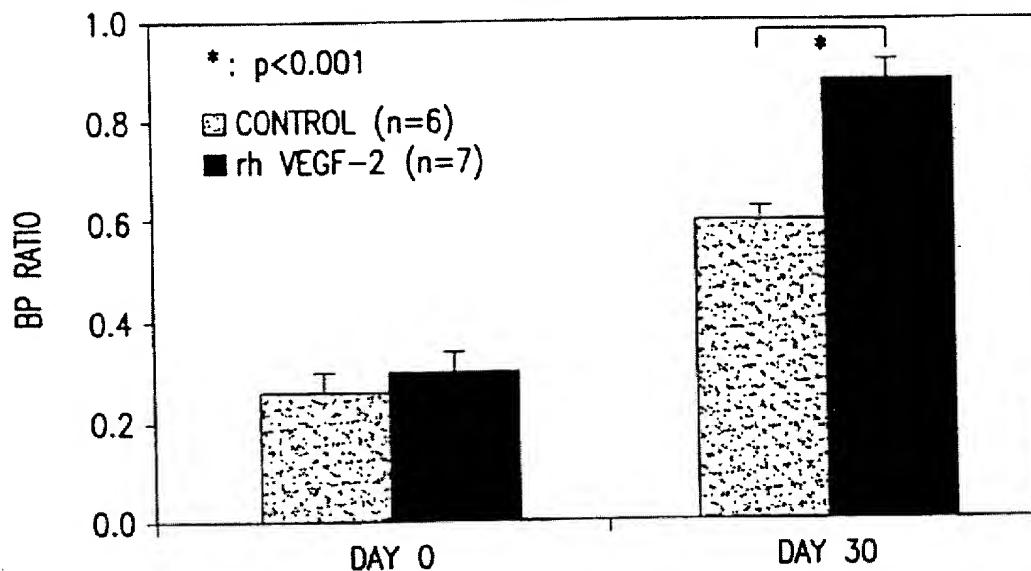


FIG. 25A

CALF BLOOD PRESSURE RATIO  
-PLASMID-

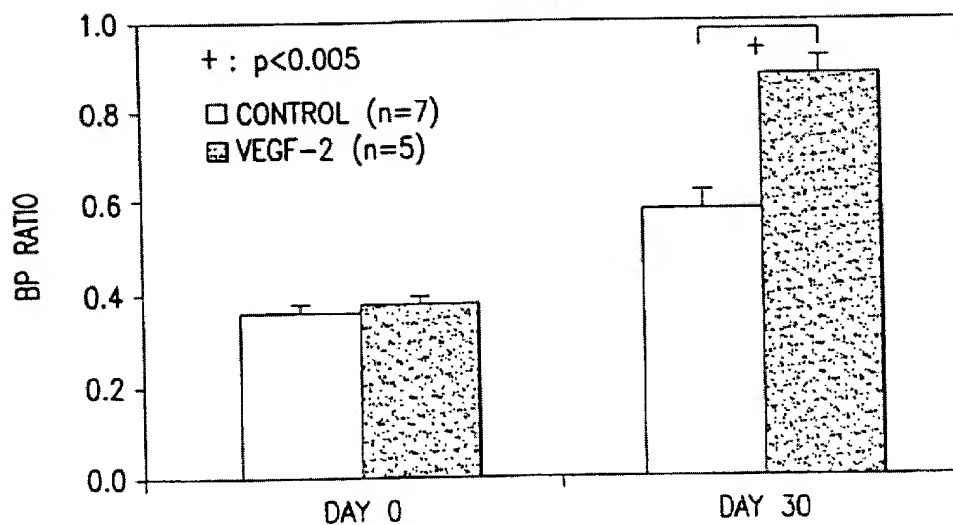


FIG. 25B

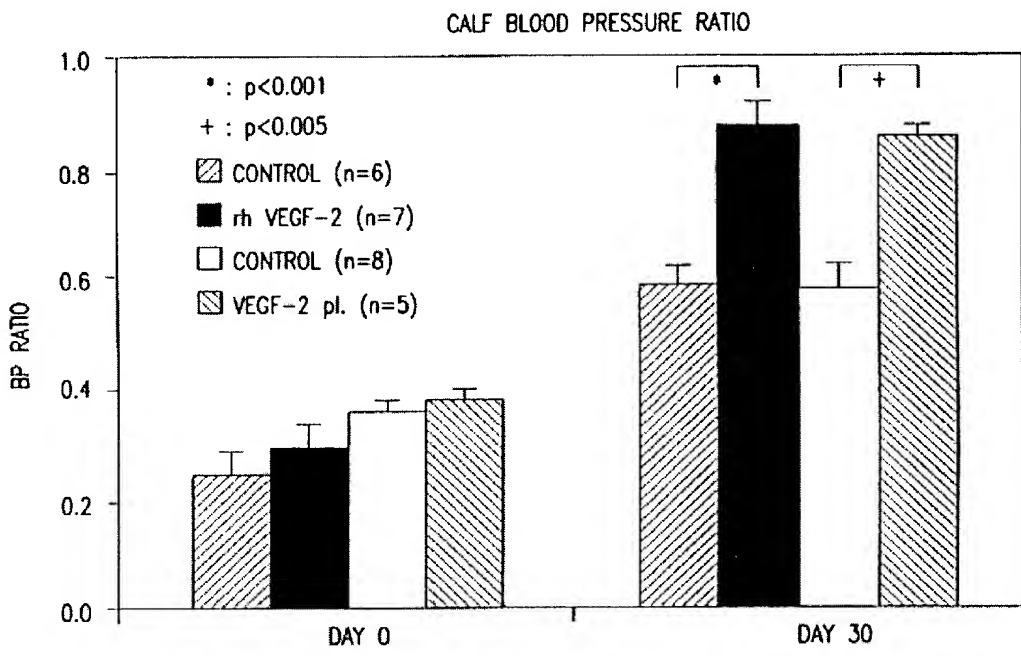


FIG. 25C

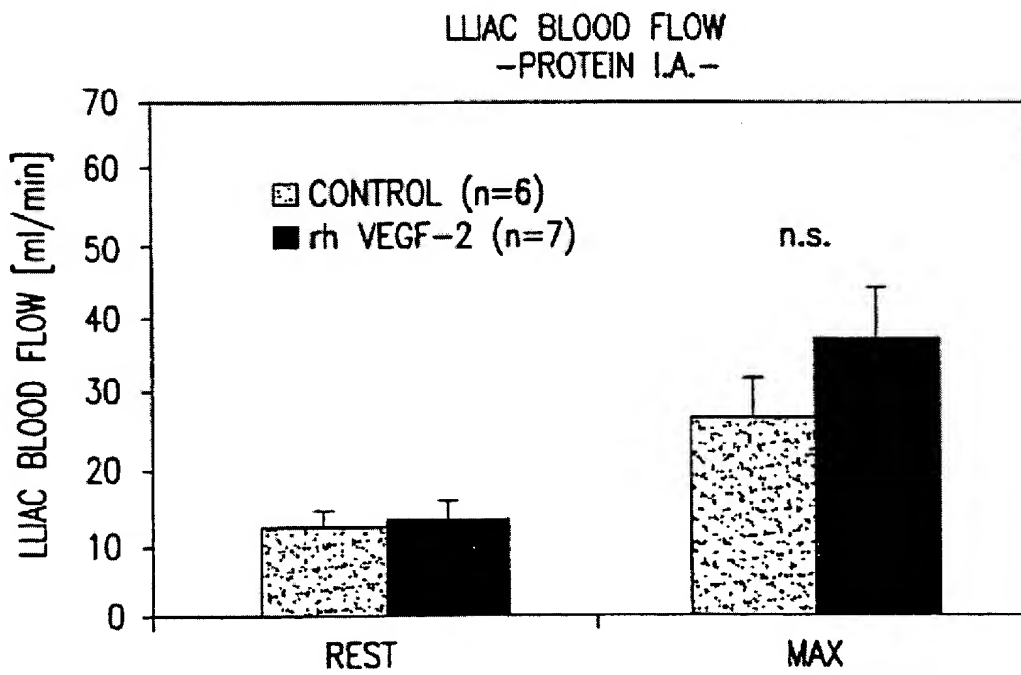


FIG. 25D

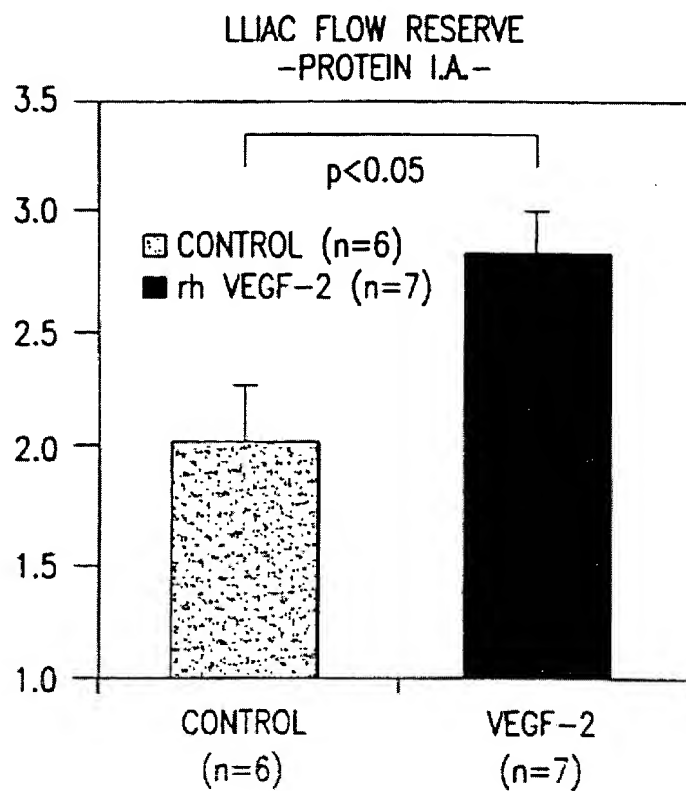


FIG. 25E

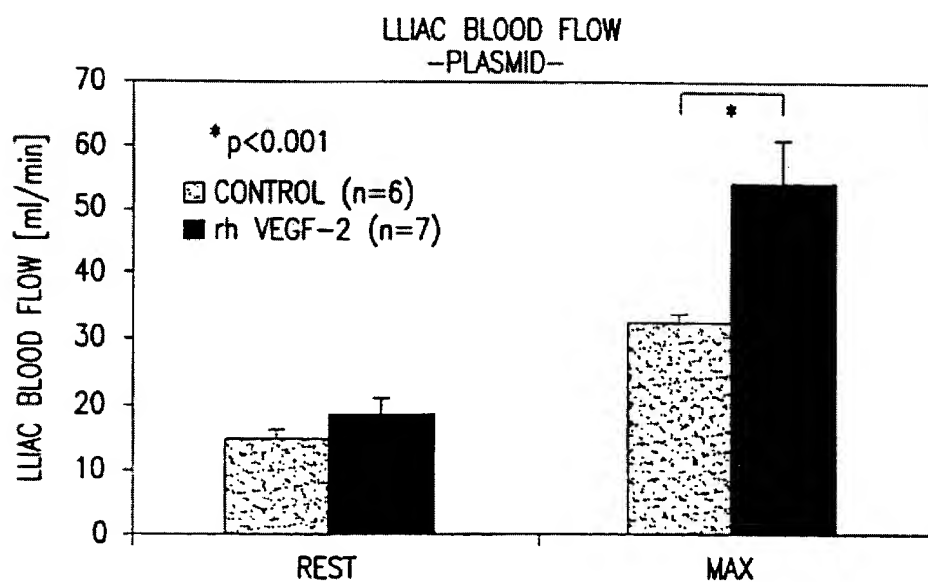


FIG. 25F

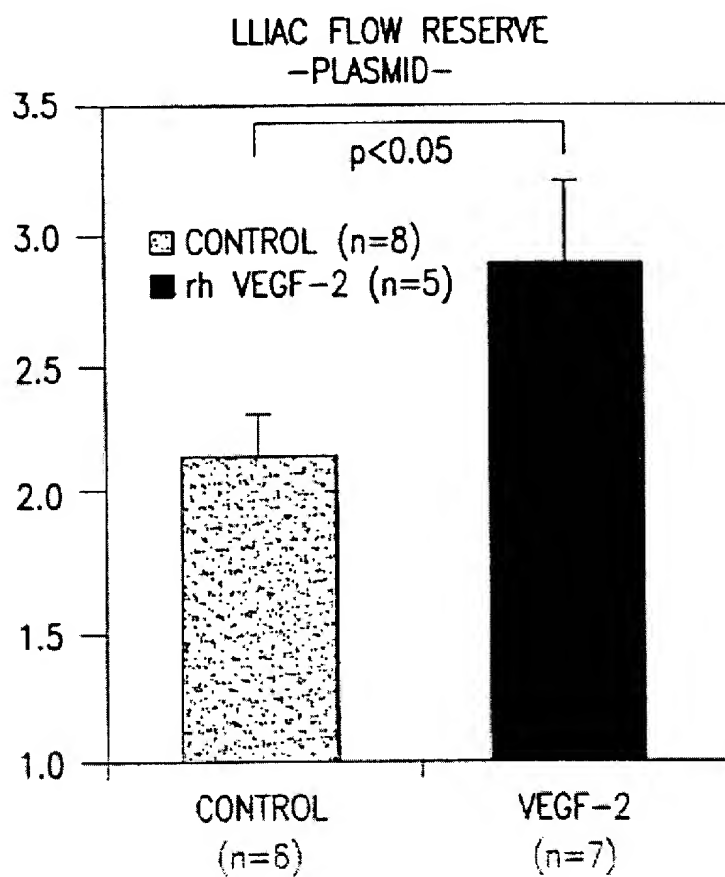


FIG. 25G

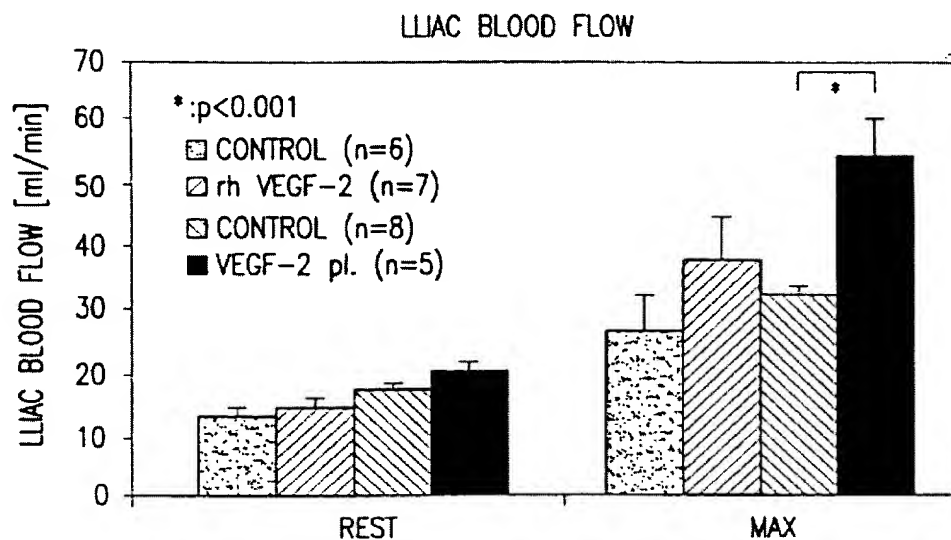


FIG. 25H

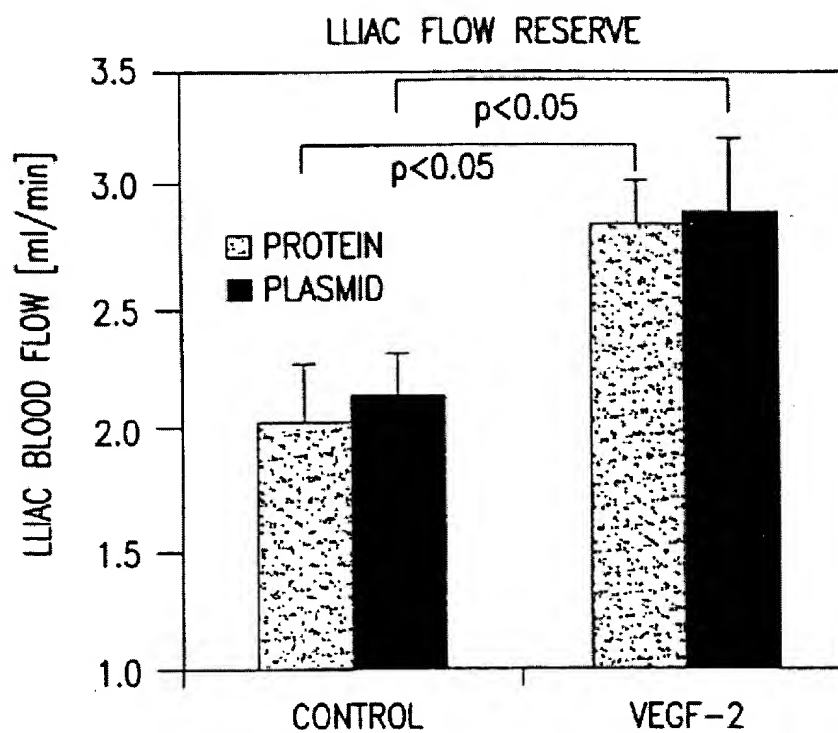


FIG. 25I

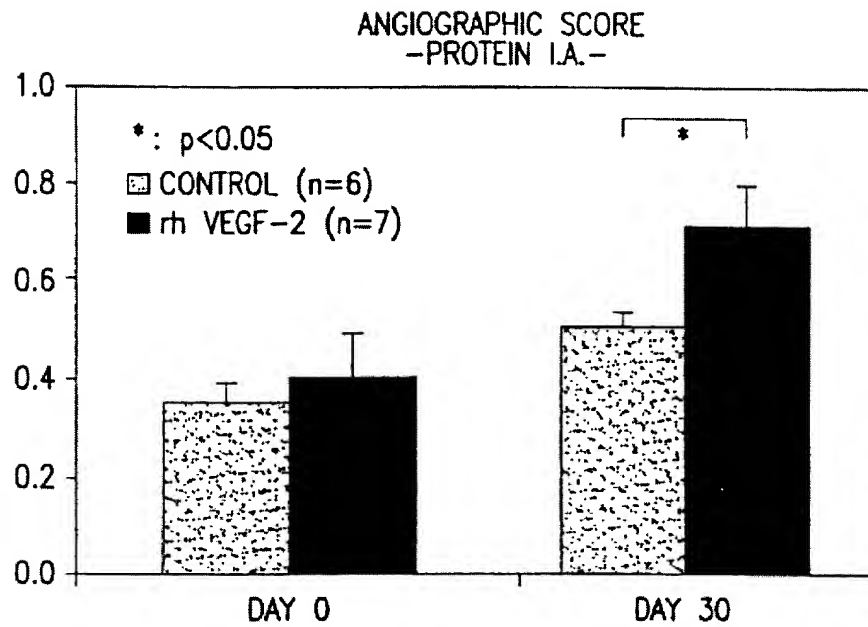


FIG. 25J

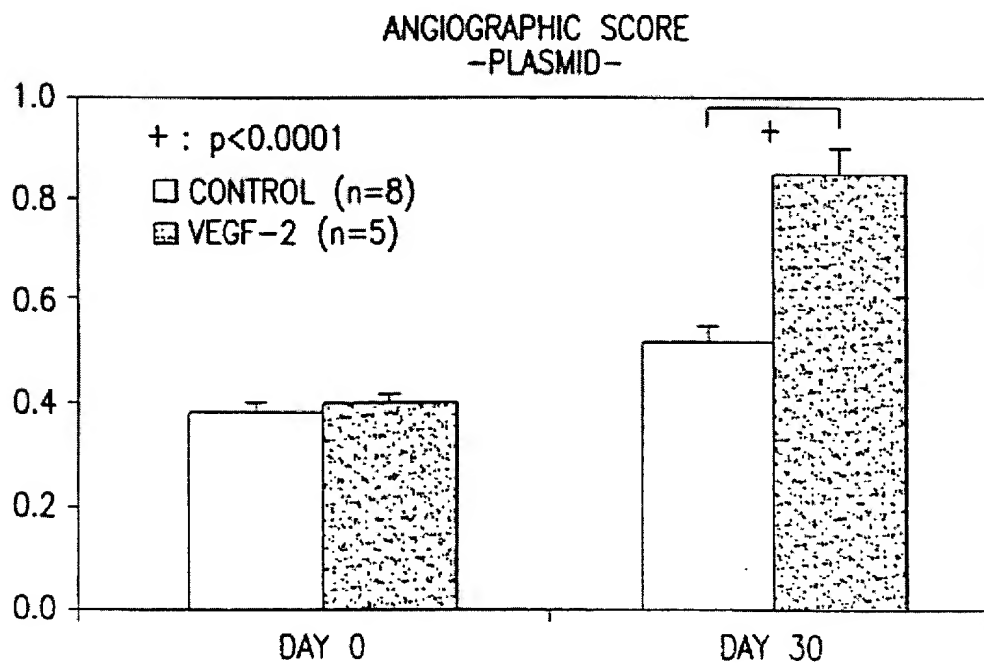


FIG. 25K

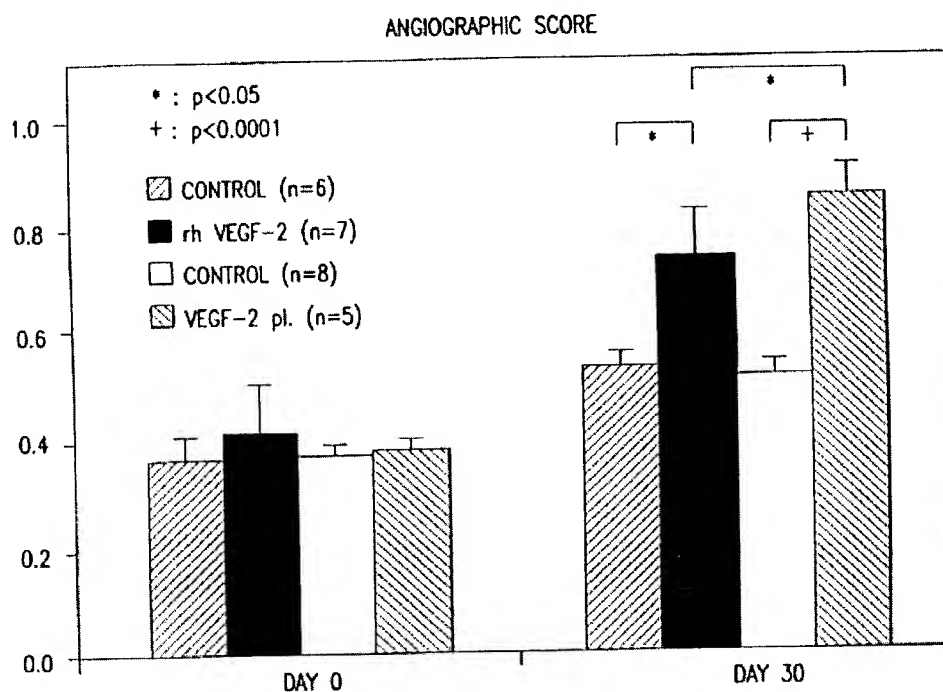


FIG. 25L

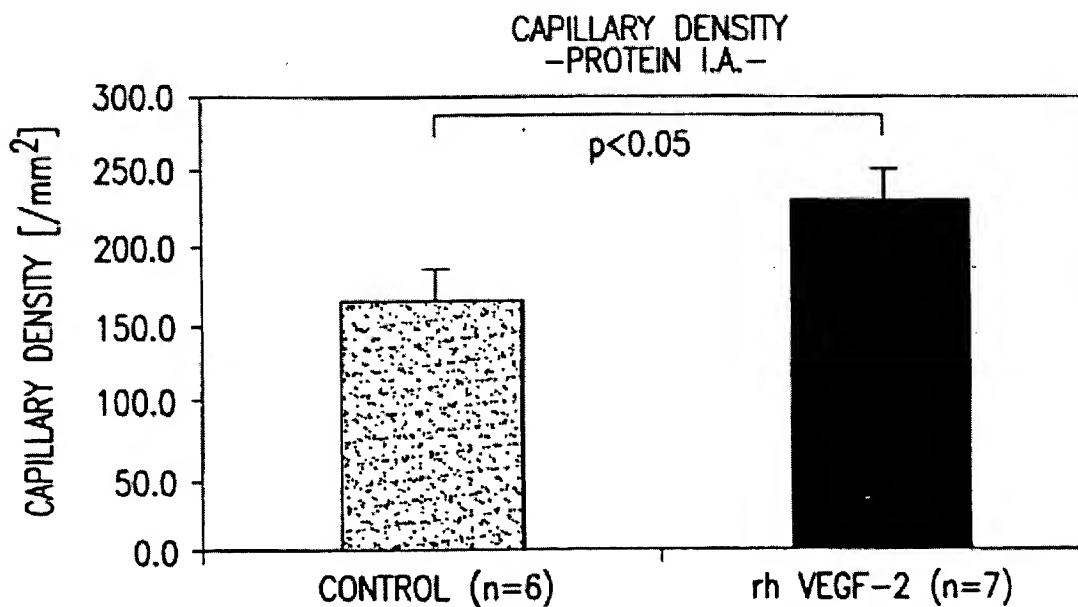


FIG. 25M

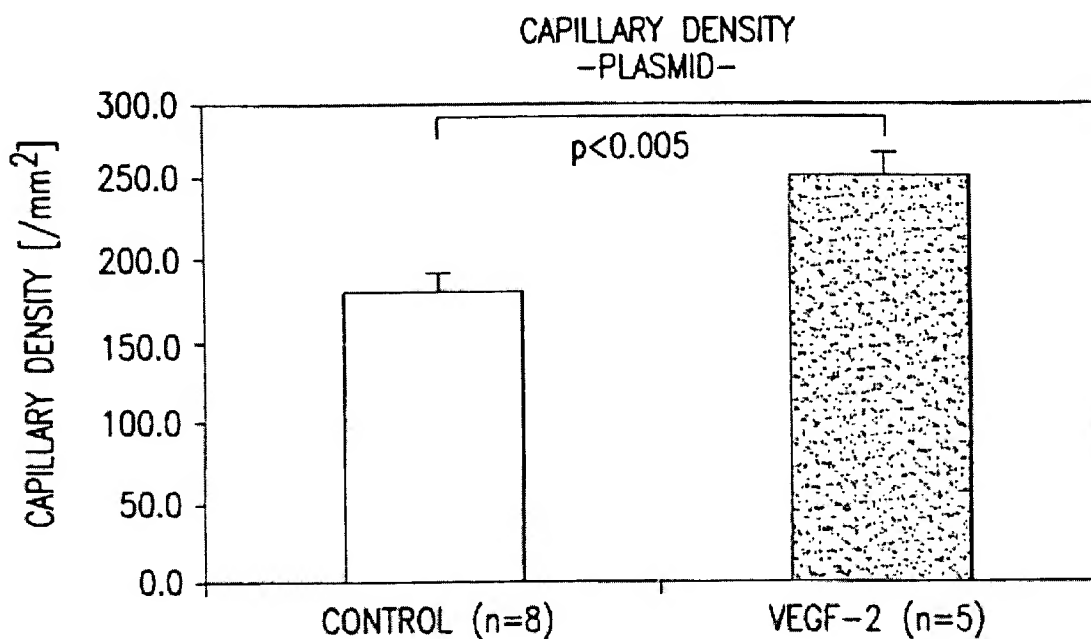


FIG. 25N

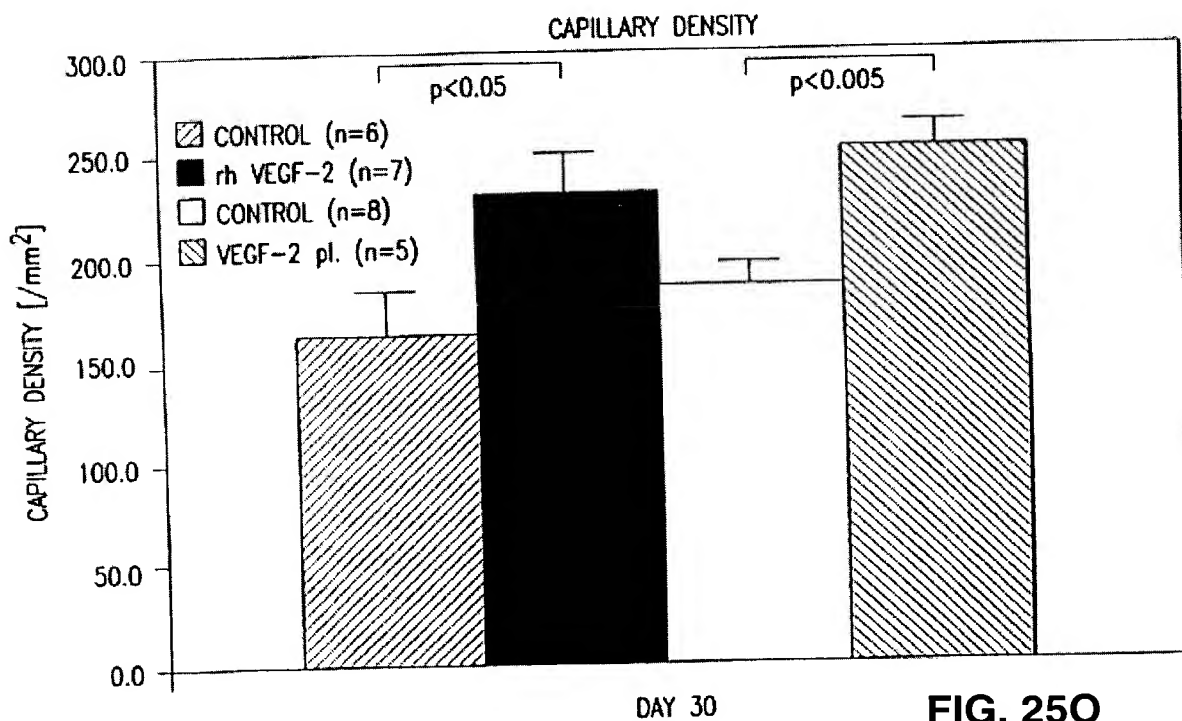


FIG. 25O



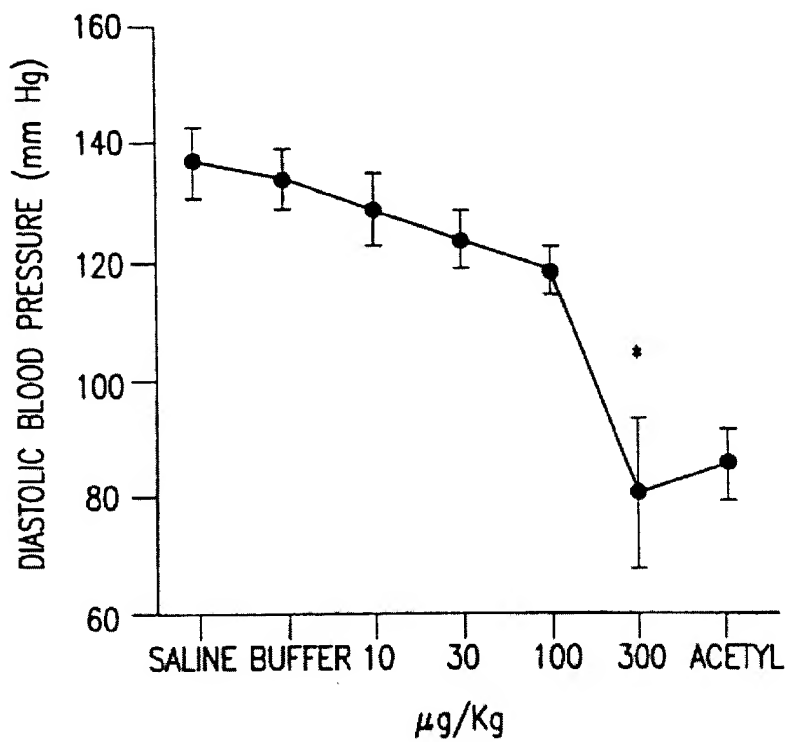


FIG. 26A

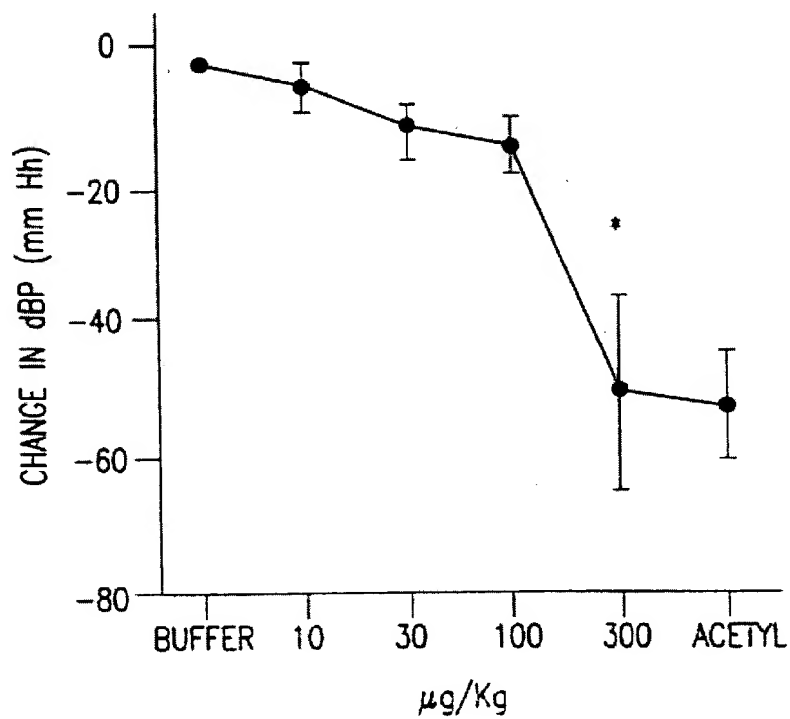


FIG. 26B

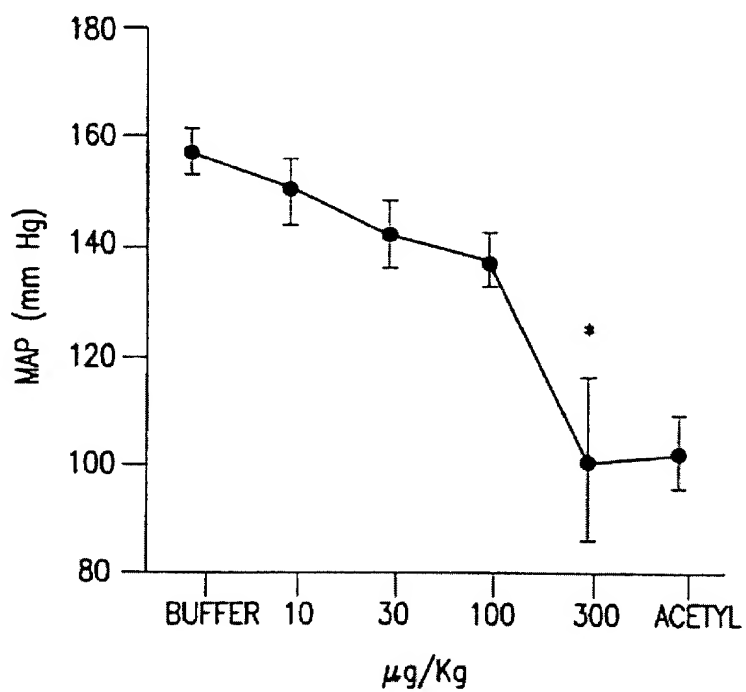


FIG. 26C

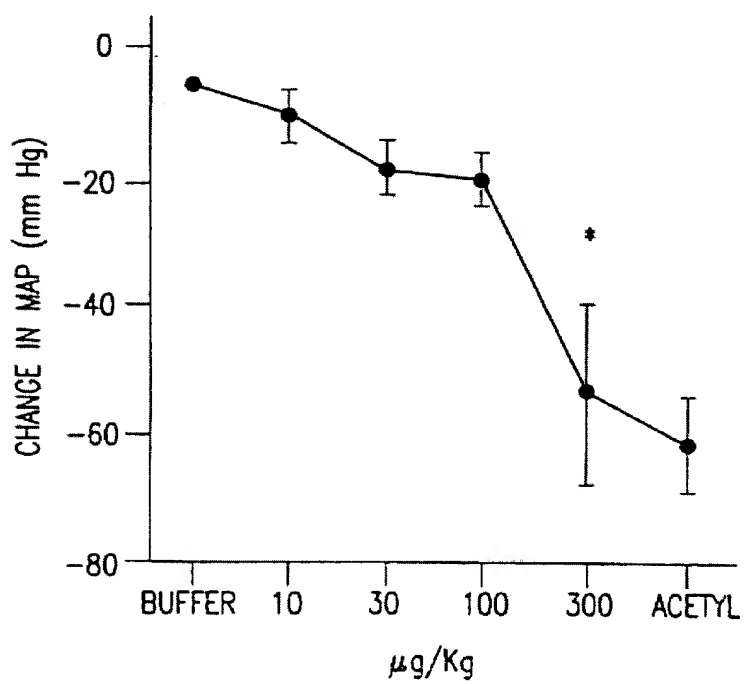


FIG. 26D

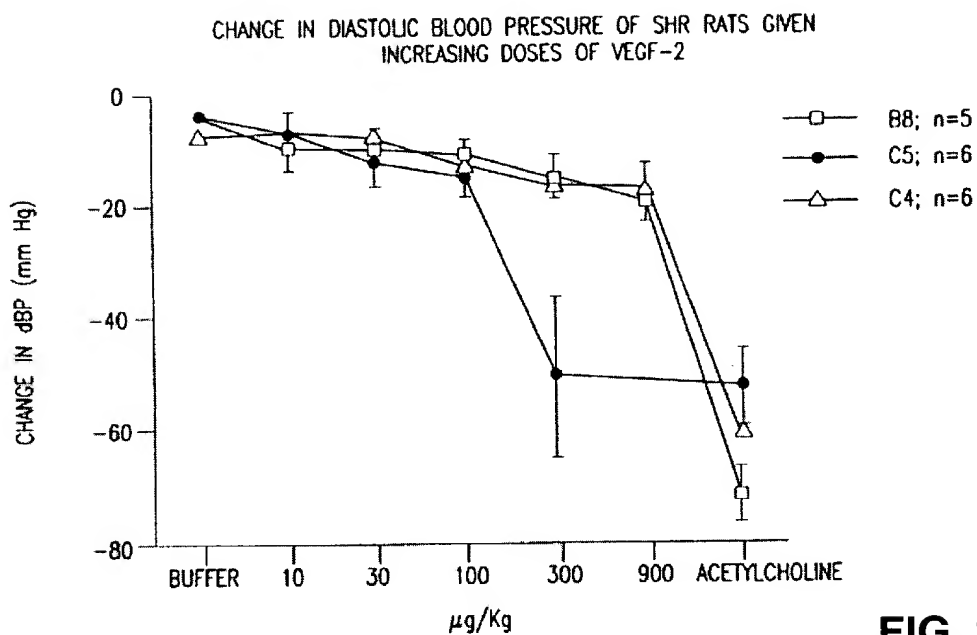


FIG. 26E

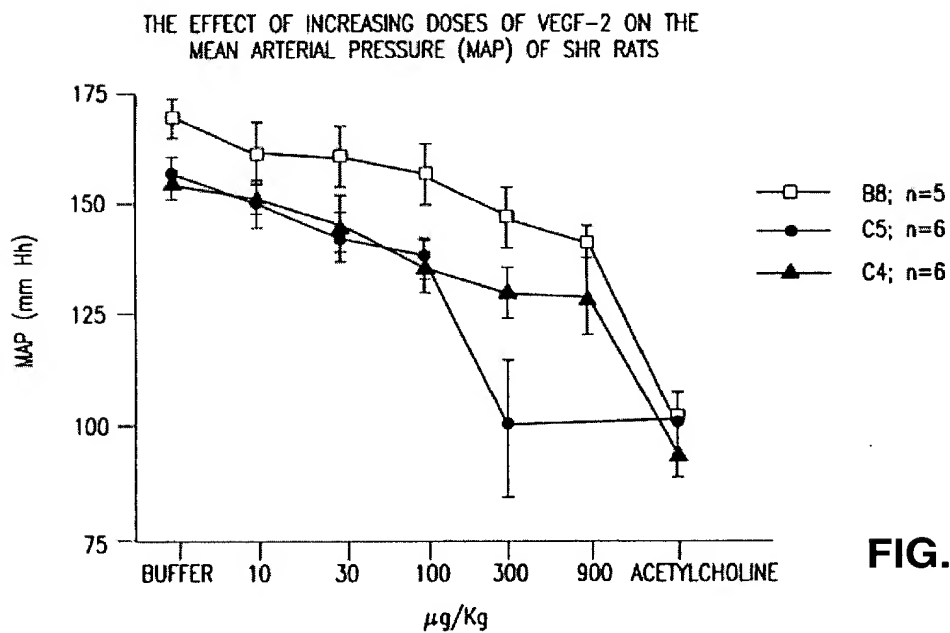


FIG. 26F

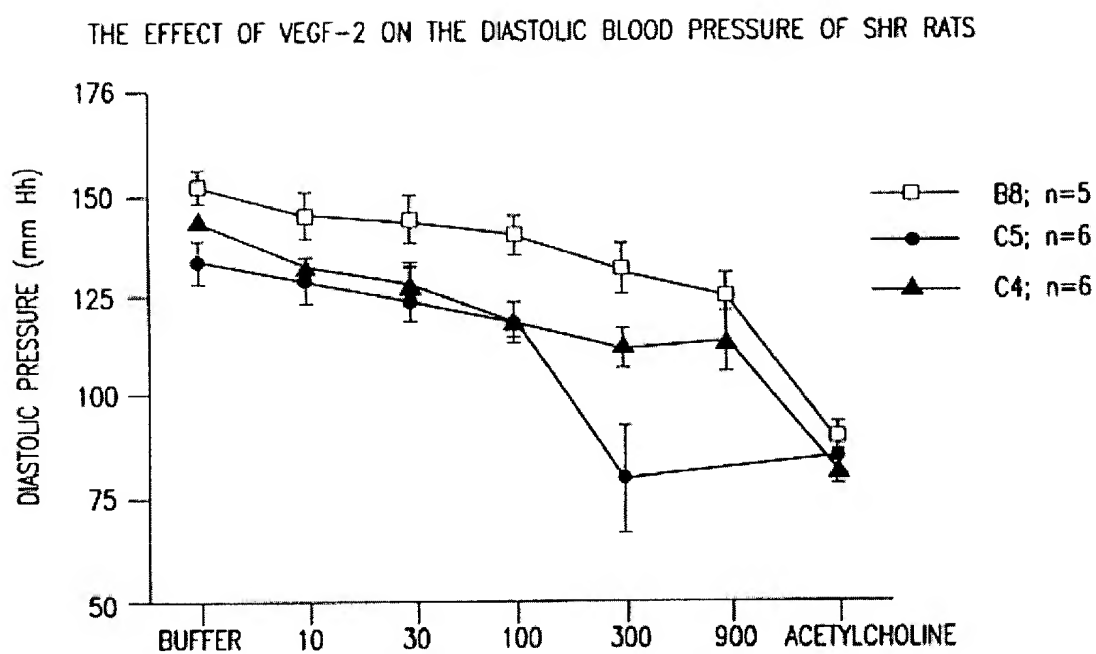


FIG. 26G

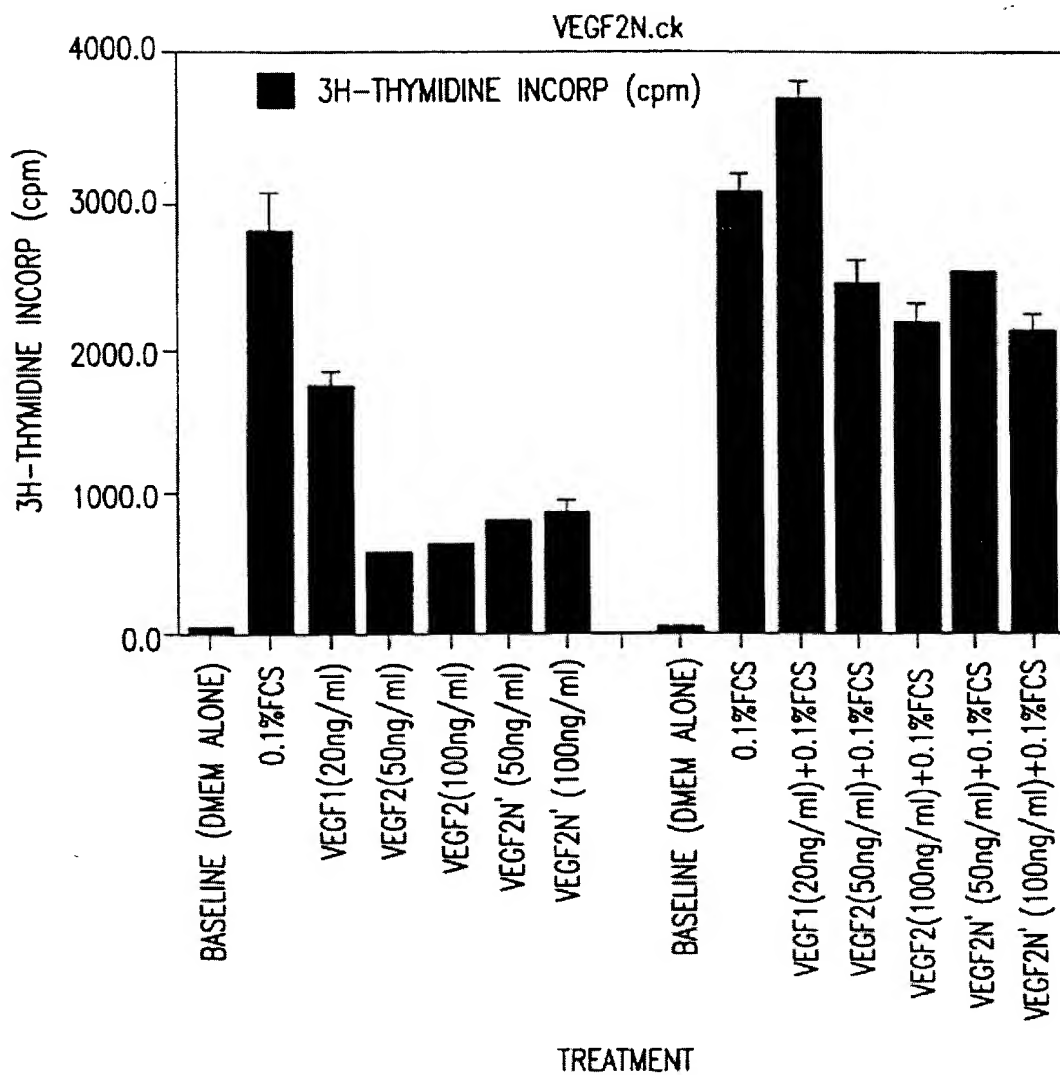


FIG. 27

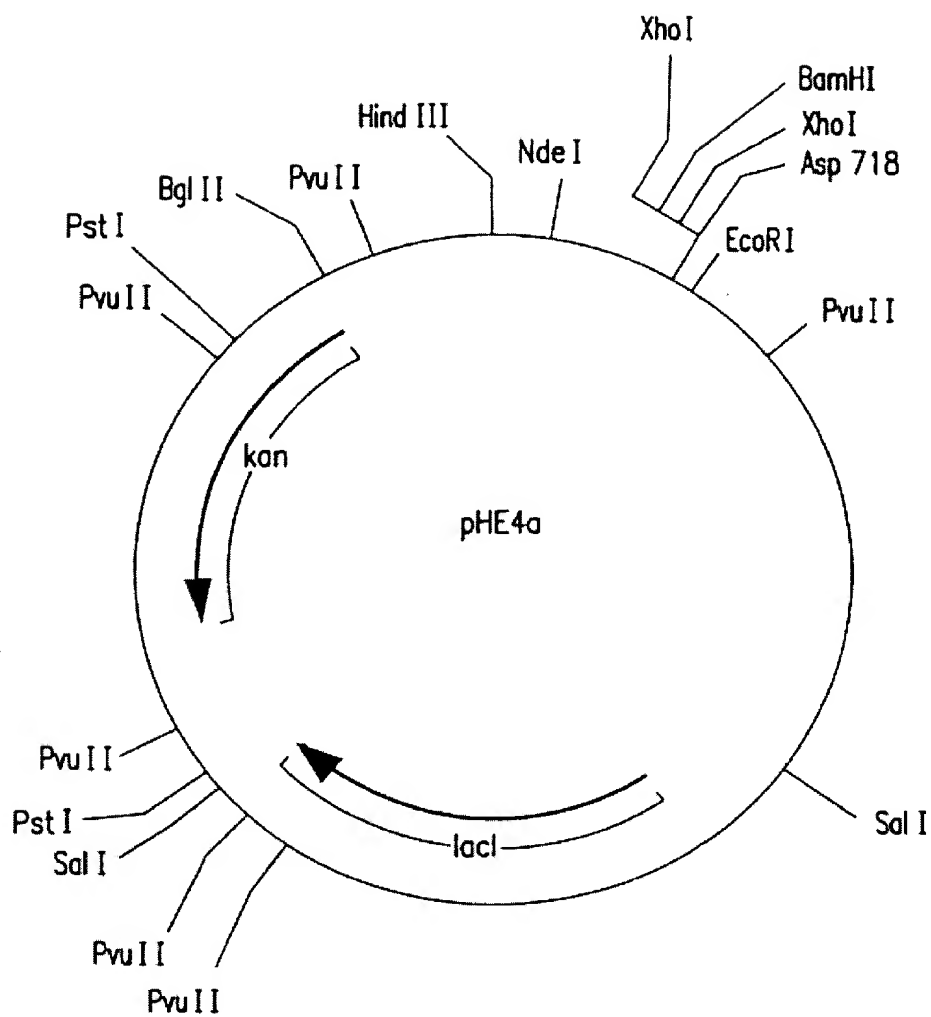


FIG. 28

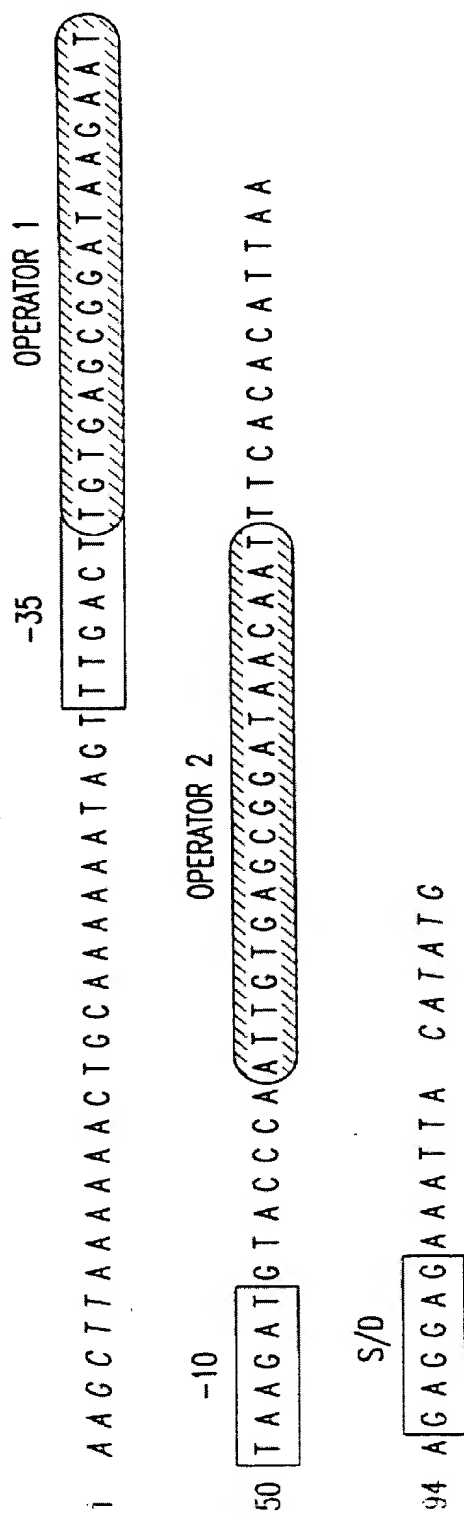


FIG. 29

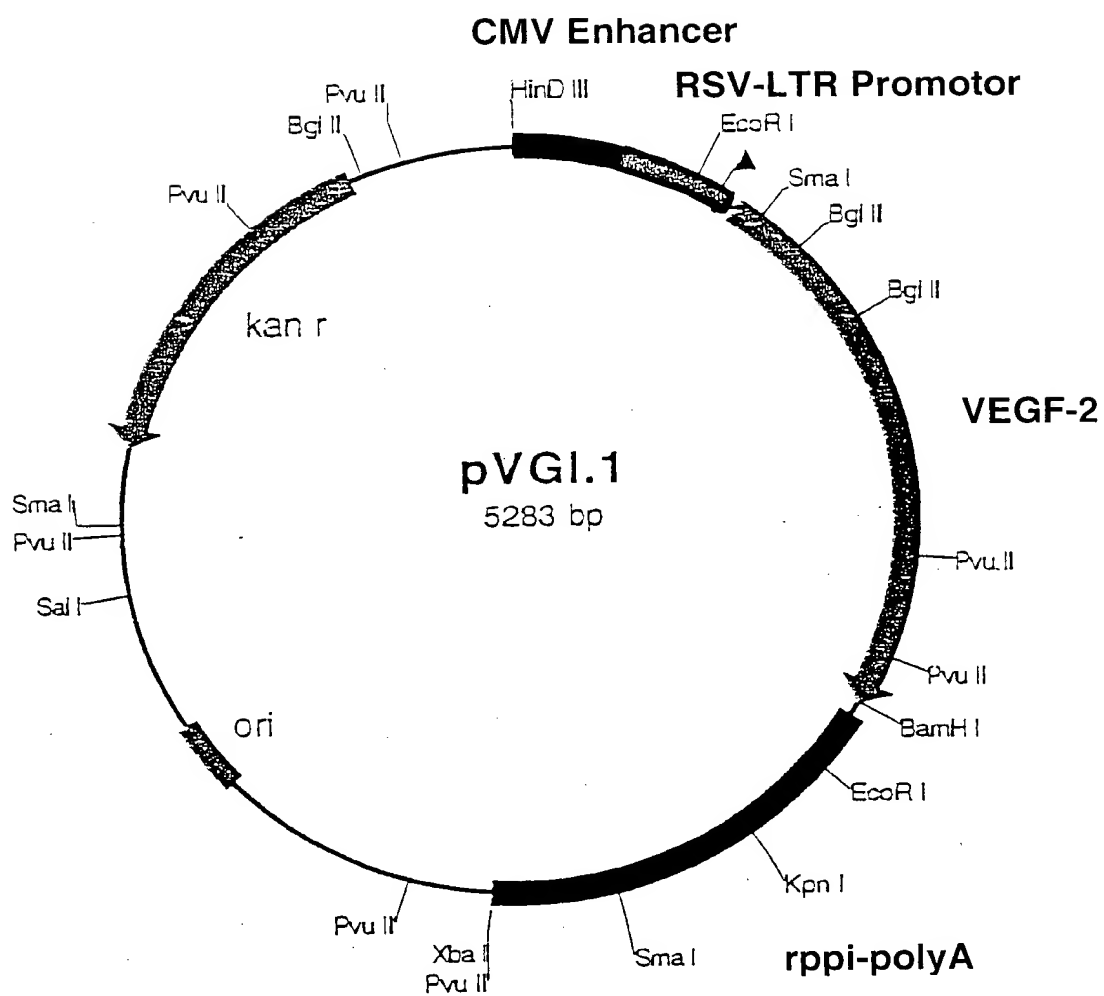


FIG. 30



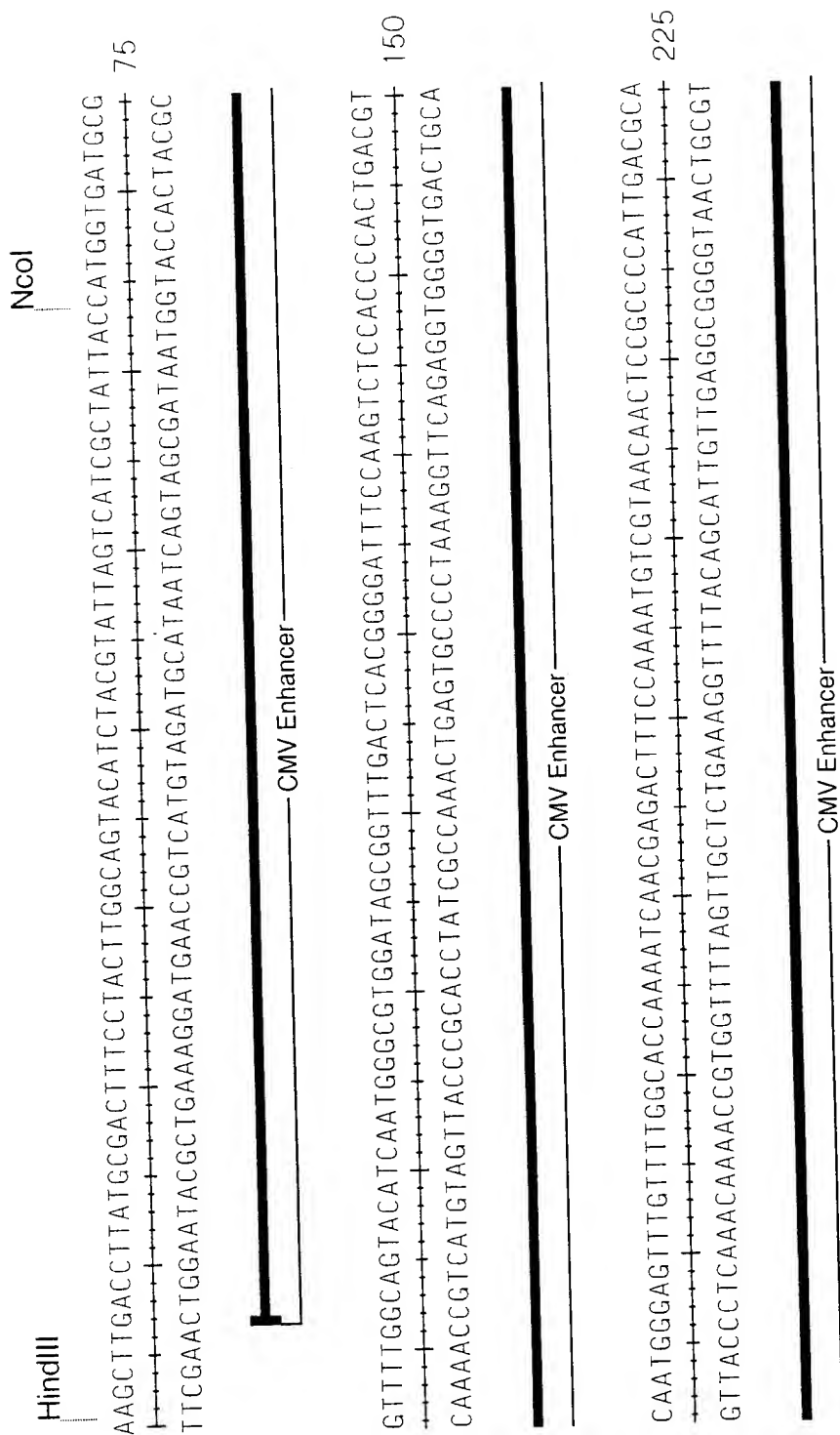


FIG.31A

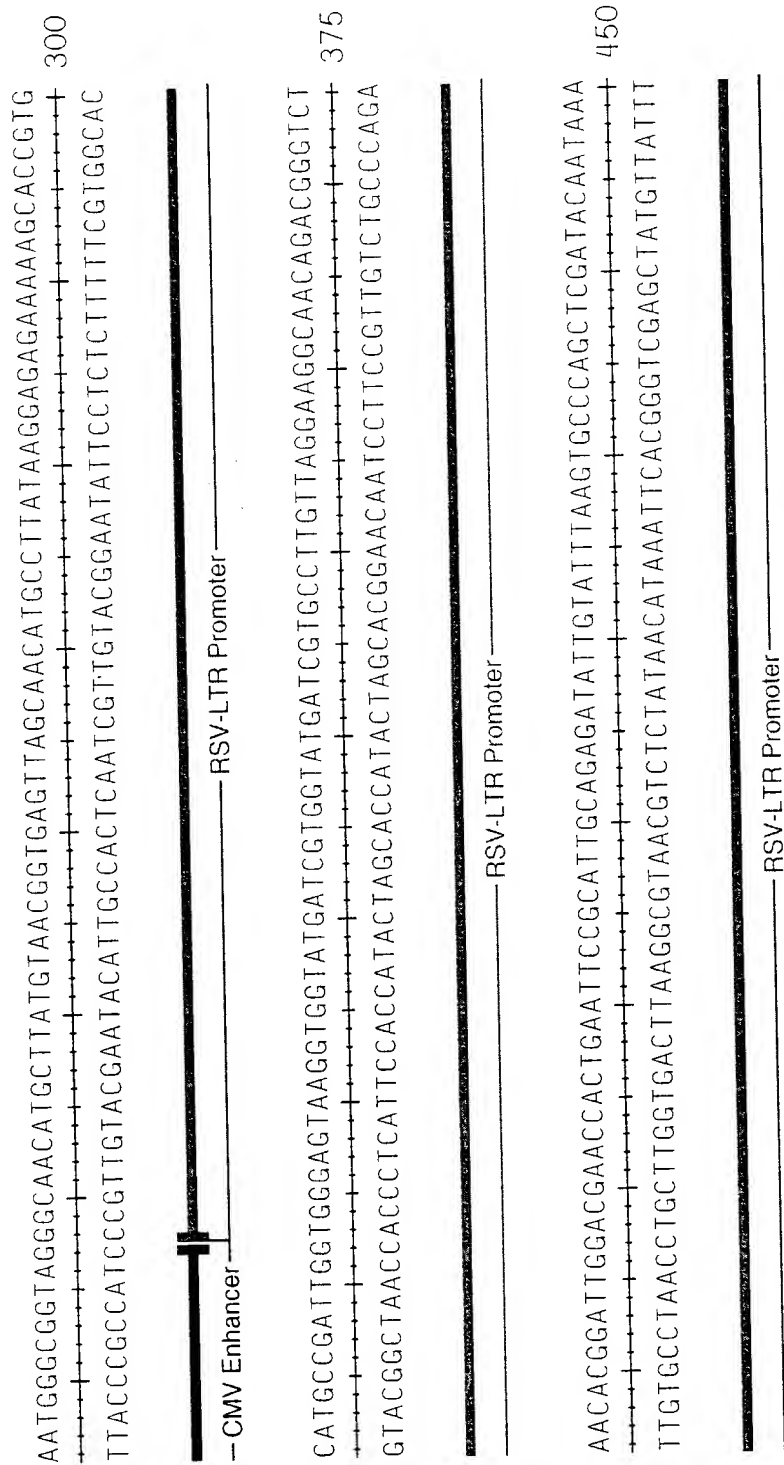


FIG.31B

CGCCATTGACCATTCACCACATTTGGTGTGCACCTGGGTGGGATCGATCCATGCACATCGCTGGGCTTCTTC 525  
GCGGTAAACTGGTAAGTGGTGTAAACACACACGTGGACCCCAACCTAGCTAGGTAGTACGTGAGCGGACCCGAAGAAG

RSV-LTR Promoter

M H S L G F F  
VEGF-2

SmaI

TCTGTGGCGTGTTCCTGCTGCGCGCTGCTCCCGGGTCTCGCGAGGCGCCCGCGCGCGCCCTTC 600  
AGACACCGCACAAAGAGACGAGCGGCGACGCGGAGGCGCCAGGAGCGCTCCGCGGGCGCGCGCGCGGAAG

S V A C S L L A A A L L P G P R E A P A A A A F  
VEGF-2

BglII

GAGTCCGGACTCGACCTCTCGGACGCGGAGCCCGACGCGGGTGAGGCCACGGCTTATGCAAGCAAAGATCTGGAG 675  
CTCAGGCCCTGAGCTGGAGAGCCTGCGCCTCGGGCTGCGGCCCACTCCGGTGCCGAATACGTTCTTAGACCTC

E S G L D L S D A E P D A G E A T A Y A S K D L E  
VEGF-2

FIG.31C

GAGCAGTTACGGTCTGTGCCAGTGTAGATGAACATCATGACTGTACTCTACCCAGAATAATTGGAAAAATGTACAAG  
CTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTTATAACCTTTTACATGTTT  
750

---

E Q L R S V S S V D E L M T V L Y P E Y W K M Y K  
VEGF-2

---

TGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAAGAGACTATA  
ACAGTCGATTCCCTTCCCTCCGACCGTTGTATIGTCTCTTGTCGGTGGAGTTGAGTTCCCTGCTTCTCTGATAT  
825

---

C O L R K G G W O H N R E Q A N L N S R T E E T I  
VEGF-2

---

AAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAAATGAGTGGAGAAAGACATCAATGCAIG  
TTTAAACGACGTCGTGTAATATTATGTCCTAGAACCTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTAC  
900

---

K F A A A H Y N T E I L K S I D N E W R K T O C M  
VEGF-2

FIG.31D

CCACGGGAGGIGTGATAGATGTGGGAAGGAGTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCAIGTGTG 975  
GGTGCCCTCCACACATATCTACACCCCTTCCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACACAC  
P R E V C I D V G K E F G V A T N T F F K P P C V  
VEGF-2

PstI  
TCCGTCTACAGATGTGGGGTGTGCTGCAATAGTGAGGGGCTGCAGTGCAATGAACACCCAGCAGCTACCTCAGC 1050  
AGGCAGATGCTACACCCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGTCGTGCTCGATGGAGTCG  
S V Y R C G C C N S E G L Q C M N T S T S Y L S  
VEGF-2

AAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTTGCCAAATCACACT 1125  
TTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCGGGGTTTGGTCATTGTTAGTCAAAACGGTTAGTGTGA  
K T L F E I T V P L S Q G P K P V T I S F A N H T  
VEGF-2

FIG.31E

1200  
TCCTGCCGATGCTAAGTGGATGTTTACAGACAAGTTCCATTATTAGACGTTCCCTGCCAGCAACA  
AGGACGGCTACGTACAGATTGACCTACAAATGCTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCTGTGT  
-----  
S C R C M S K L D V Y R Q V H S I I R R S L P A T  
-----VEGF-2

PstI

1275  
CTACCACAGTGTACGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACAATCTGCAGATGCCCTG  
GATGGTGTACAGTCCGTGCTTCTGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGCTCTACGGAC  
-----  
L P Q C Q A A N K T C P T N Y M W N N H I C R C L  
-----VEGF-2

1350  
GCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCA  
CGAGTCCTTCTAATAACAAAAGGAGCCCTACGACCTCTACTGAGTTGCTCTACCTAAGTACTGTAGACACCTGGT  
-----  
A Q E D F M F S S D A G D D S T D G F H D I C G P  
-----VEGF-2

FIG.31F

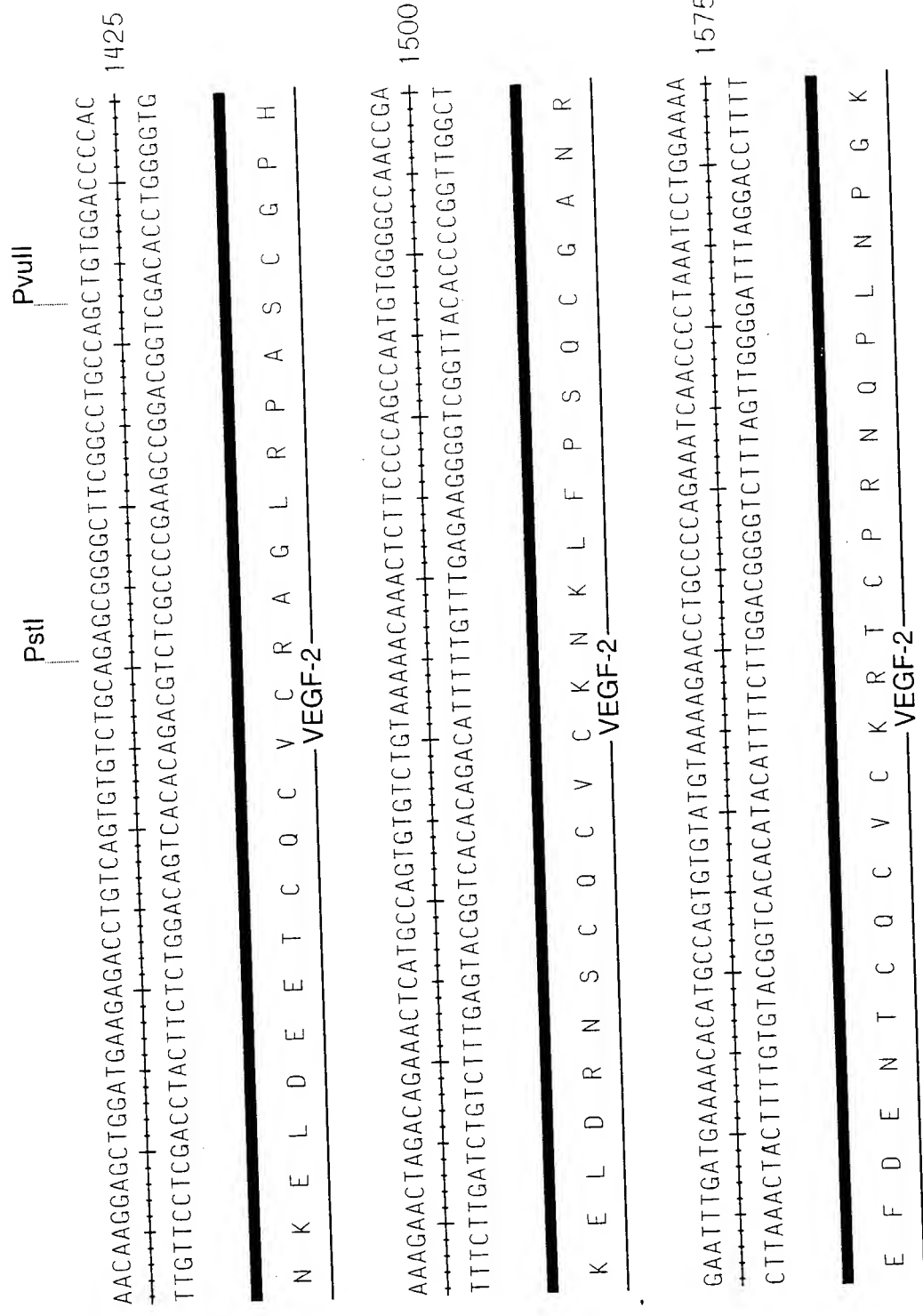


FIG.31G

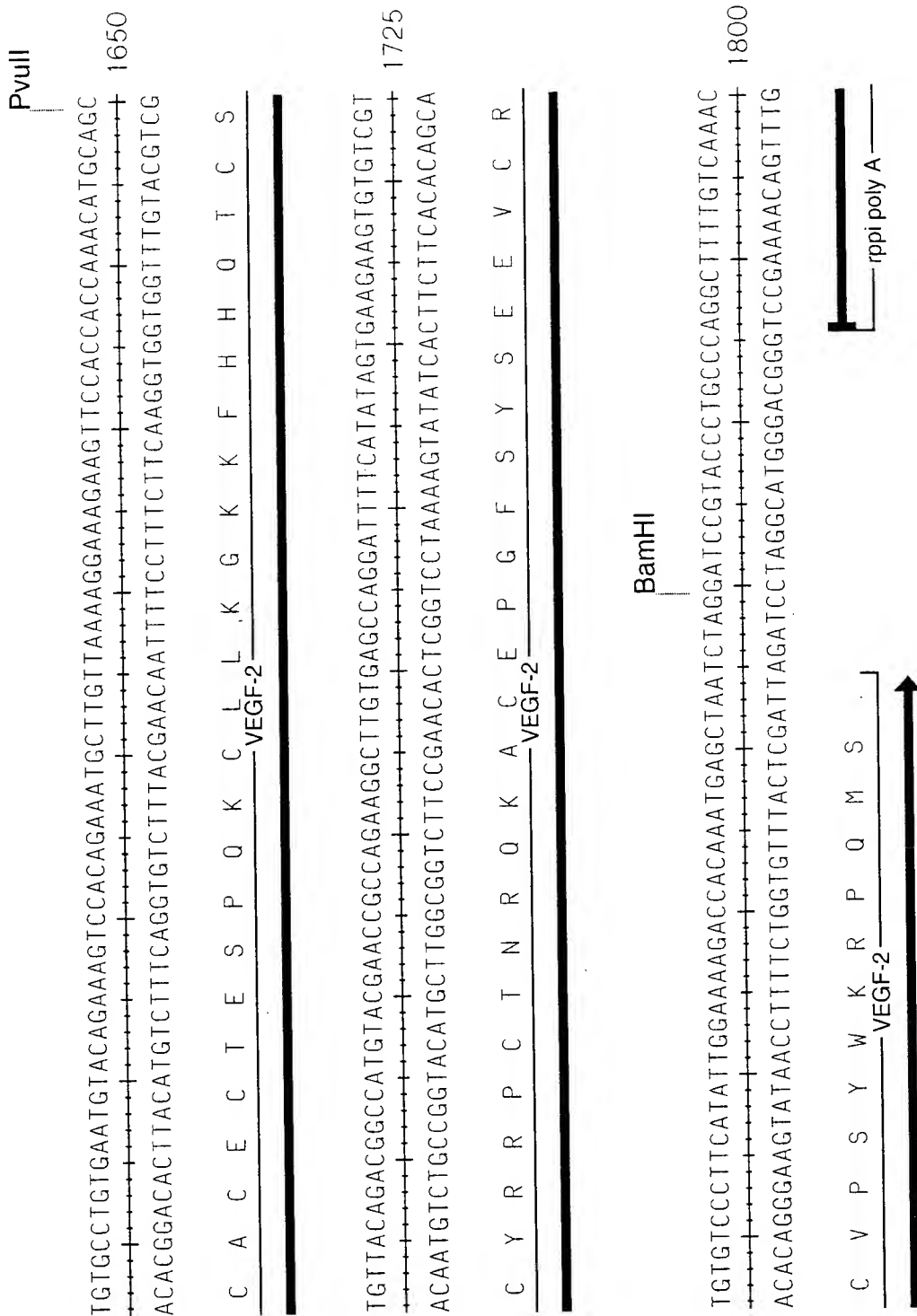


FIG.31H



1875  
AGCACCTTTGTGGTTCTCAGTGGTGGAAAGCTCTCTACCTGGTGTGGGGAGCGTGGATTCTTCTACACACCCA  
TCGTGGAACACCAAGAGTGAACCACTTCGAGAGATGGACCACACACACCCCTCGCACCTAAGAAGATGTGTGGGT  
-----  
----- rppi poly A -----  
  
1950  
TGTCCCGCGGAAGTGGAGGACCCACAAGGTAAGCTCTGCTCCTGAATTCTATCCCAAGTGCTAACTACCTGT  
ACAGGCGGCGCTTCACCTCCTGGGTGTTCCATTGAGAGCGAGGACTTAAGATAGGGTTCACGATTGATGGGACA  
-----  
----- rppi poly A -----  
  
2025  
TTGTCTTTCACCCCTTGAGACCTTGTAATTTGTGCCCCCTAGGTGTGGAGGGTCTCAGGCTAACCAGTGGGGGCACA  
AACAGAAAGTGGGAACCTCTGGAACATTTAACACGGGATCCACACCTCCCGAGAGTCCGATTGGTCACCCCCCGTGT  
-----  
----- rppi poly A -----

FIG.31I

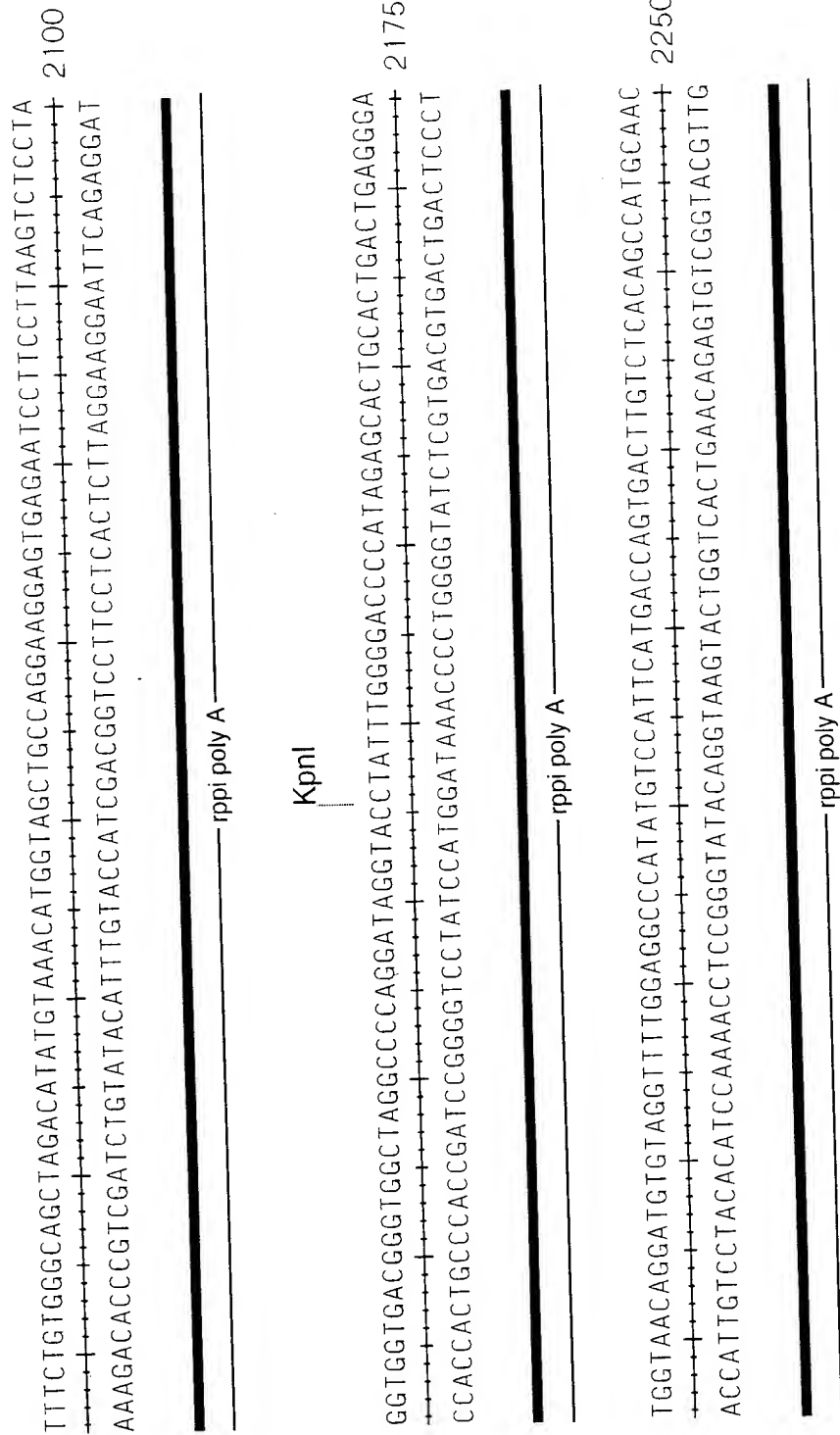


FIG.31J

2325  
CCTTGCCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTGGGCTAATCAGGGGGTCGCTCAGCTCC  
+-----+  
GGAACGGAGGACACGACTGAATCGTCCCCTATTTCACCTCTCTTTCGGACCCGATTAGTCCCCCAGCGAGTCGAGG

----- rppi poly A -----

2400  
TCCTAACTGGATTGTCCCTAATGCTCTTTGCTTCTGTGCTGCTGATGCTCTGCCCCGTGCTGCTGACATGACCTCCCTG  
+-----+  
AGGATTGACCTAACAGGATACACAGAAACGAAGACACGACCTACGAGACGGGACACGACTGTACTGGAGGGAC

----- rppi poly A -----

Smal

2475  
GCAGTGGCACAAC TGGAGCTGGGTGGAGGCCCGGGGCAGGTGACCTTCAGACCTTGGCACTGGAGGTGGCCCGG  
+-----+  
CGTCACCGTGTGACCTCGACCCACCTCCGGGGCCCCCGTCCACTGGAAGTCTGGAAACCGTGACCTCCACCCGGGCC

----- rppi poly A -----

2550  
CAGAAAGCGCGGCATCGTGGATCAGTGTGCACCAGCACTCTGCTCTCTCTACCAACTGGAGAAGTACTGCAACTAG  
+-----+  
GTCTTCGGCGCGGTAGCACCTAGTCACGACGTGGTCGTAGACGAGAGAGATGGTTGACCTCTTGATGACGTTGATC

----- rppi poly A -----

FIG.31K

2625  
GCCCACTACCTGTCCACCCCTCTGCAATGAATAAAACCTTTGAAAGAGCACTACAAGTTGTGTACATGC  
CGGGTGGTGAATGGGACAGGTGGGGAGACGTTACTTATTTTGGAACTTTCTCGTGATGTTCAACACACATGTACG

— rppi poly A —

2700  
GTGCATGTGCATATGTGGTGGGGGGAACATGAGTGGGGCTGGCTGGAGTGGTCGGGCTTAATCTATCTGGCA  
CAGTACACGTATACACCAGGCCCCCTTGTACTCACCCTGACCGACCTCACCAGCGCGAATTAGATAGACCGT

— rppi poly A —

PvuII XbaI

2775  
GCTGTCTAGACGTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTATCCGCTCACAATCCACACAACATA  
CGACAGATCTGCATTAGTACCAGTATCGACAAAGGACACACTTTAACAAATAGGCGAGTGTAAAGGTGTGTAT

2850  
CGAGCCGGAAGCATAAAGGTAAAGCCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAAATTCGCTTGCCTCA  
GCTCGGCCTTCGTATTTACATTTTCGGACCCACGGATTACTCACTCGATTGAGTGTAAATTAACGCAACGCGAGT

FIG.31L

PvuII

CTGCCCCGCTTTCAGTCGGGAACCTGTCGTGCCAGCTGCATTAAATGAATCGGCCAACGGCGGGGAGAGGCGGT 2925  
GACGGCGGAAGGTCAGCCCCTTTGGACAGCACGGTCGACGTAATTACTTAGCCGGTTGCGGCGCCCTCTCCGCCA  
TTGCGTATTGGGCGCTCTTCGGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTGTTTCGGCTGCGGCGAGCGGT 3000  
AACGCATAACCCGCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACGCGCTCGCCAT  
TCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAA 3075  
AGTCGAGTGAGTTCCGCCATTATGCCCAATAGGTGCTTAGTCCCTATTGCGTCCCTTCTTGACACTCGTTTT  
GGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGCGGTTTTTCATAGGCTCCGCCCCCTGACGAG 3150  
CCGGTCGTTTTCCGGTCCCTGGCATTTTCCGGGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTC

FIG.31M

CATCAGAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCGAGCGTTTCCCCCT 3225  
GTAGTGTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCCTGATATTTCATGGTCCGCAAGGGGGA  
GGAAGCTCCCTCGTGGCTCTCCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCTTCTCCCTTCGGGA 3300  
CCTTCGAGGAGCACCGGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGAGGCCCT  
AGCGTGGCGCTTCTCATAGCTCACGCTGAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCTGGGCTGT 3375  
TCGCACCGCGAAAGAGTATCGAGTGGGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACA  
GTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAACCCGGTAAGA 3450  
CACGTGCTTGGGGGCAAGTCGGGCTGGCGACGGGAA TAGGCCATTGATAGCAGAACTCAGGTGGGCCATTCT  
CAGGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG 3525  
GTGCTGAATAGCGGTGACCGTCTCGTGGTGACCATTGTCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTC

FIG.31N

TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT 3600  
AAGAACITCACCACCGGATTGATGCCGATGTGATCTTCTTGTCATAAACCATAGACGCGGAGACGACTTCGGTCAA  
ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTC  
TGGAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTGGTGGCGACCATCGCCACCAAAAAACAAACG 3675  
AAGCAGCAGATTACGGCGCAGAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAG 3750  
TTCGTCGTCCTAATGCCGGTCTTTTTTCTAGAGTCTCTAGGAACTAGAAAAGATGCCCCAGACTGCGGAGTC  
Sall  
TGGAACGAAACACGTTAAGGGATTTTGGTCATGAGATTATCGTCGACCAAAAGCGGCCATCGTGCCTCCCCAC 3825  
ACCTTGCTTTTGAGTGCAATTCCCTAAACCACTACTCTAATAGCAGCTGGTTTCGCCGGTAGCACGGAGGGGTG

FIG.310

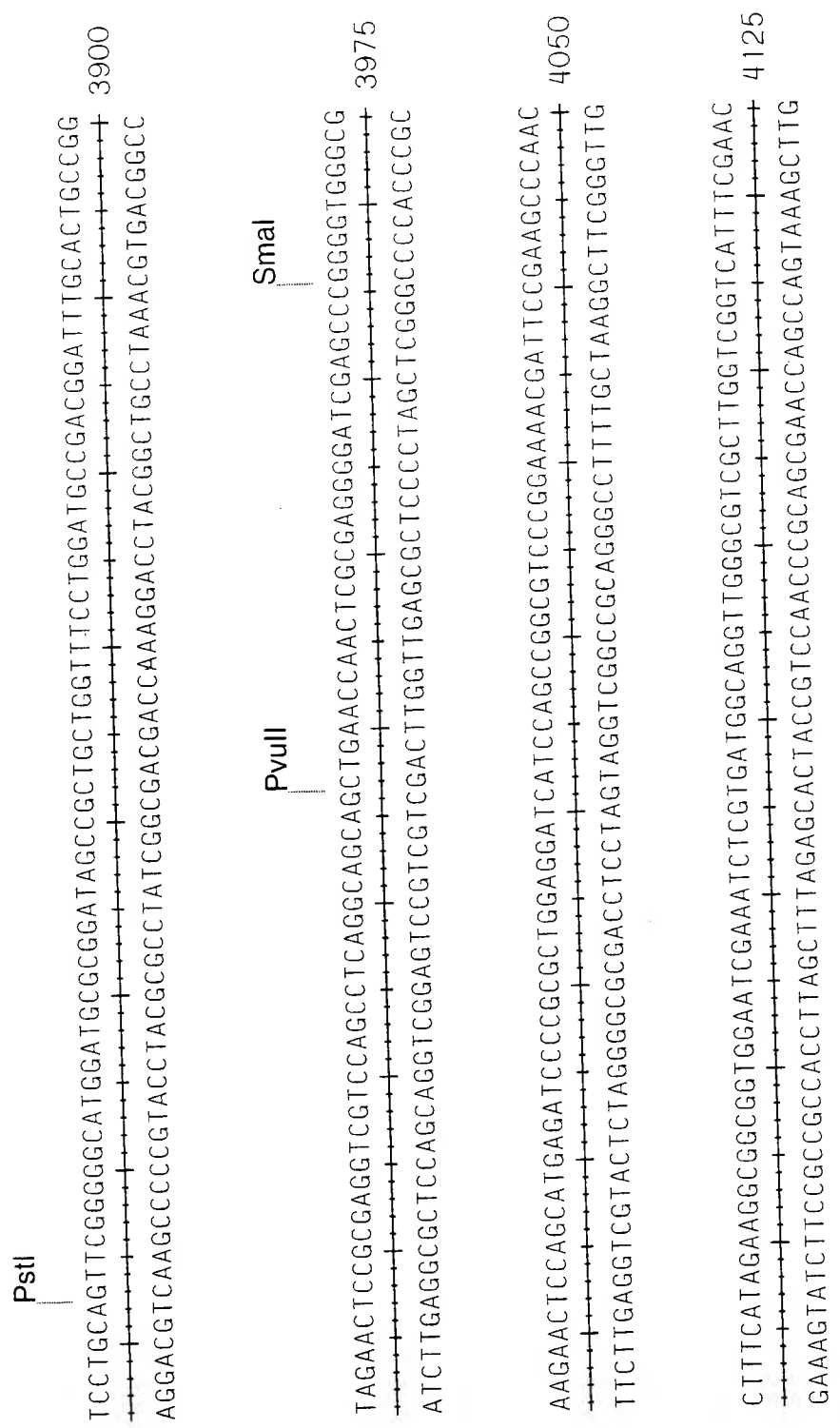


FIG.31P



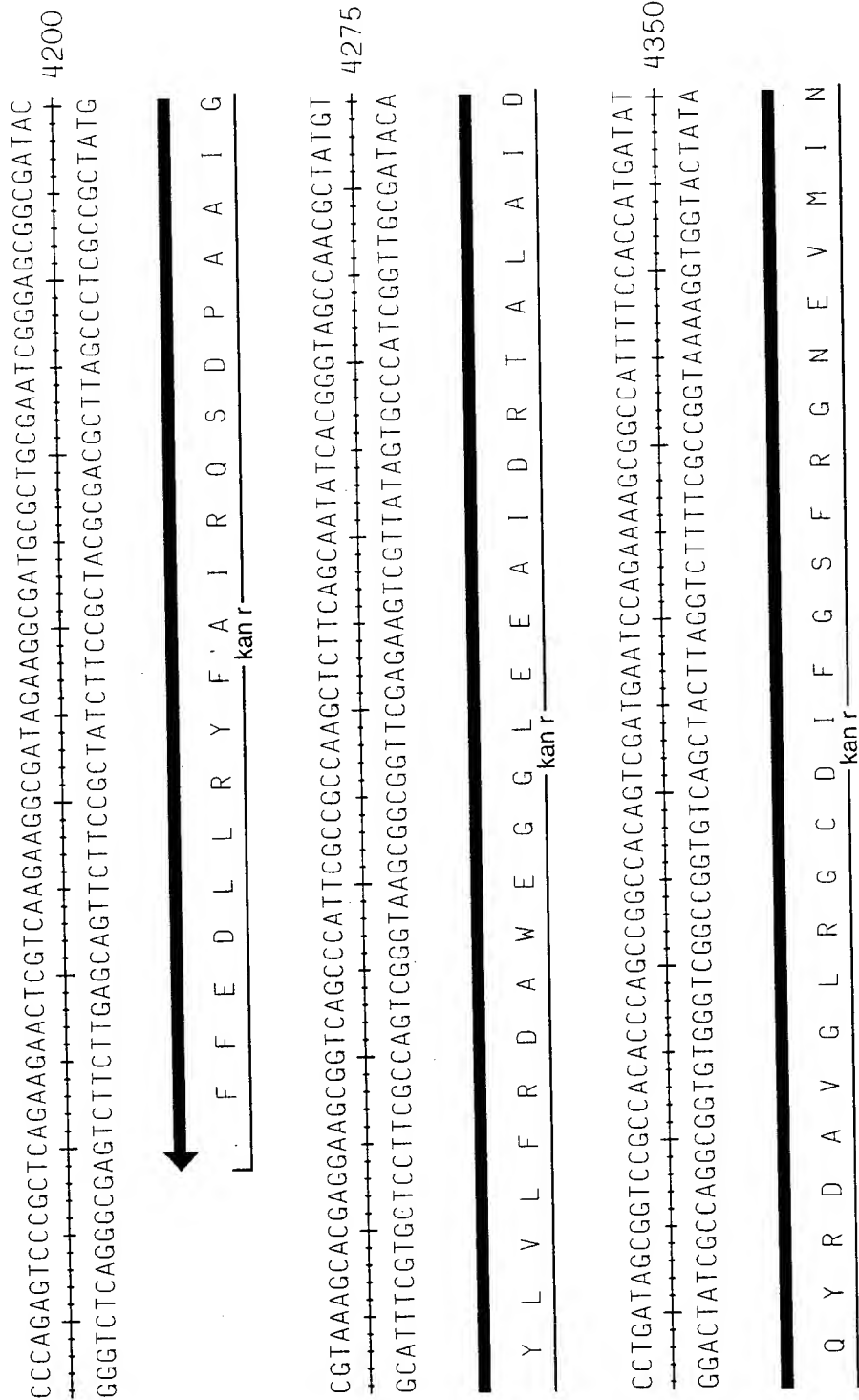


FIG.31Q

NcoI

TCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACA  
 4425  
 AGCCGTTGTCGTCGTCAGCGGTACCCAGTGTCTCTAGGAGCGGCAGCCCGTACGCGCGGAACCTCGGACCGCTTGT

P L C A D G H T V V L D E G D P M R A K L R A F L  
 kan r

GTTCGGCTGGCGGAGCCCCCTGATGCTCTTCGTCCAGATCATCTGATCGACAAGACCGGCTTCCATCCGAGTAC  
 4500  
 CAAGCCGACCGGCTCGGGGACTACGAGAAGCAGGCTAGTACTAGTGTCTGCGCGGAAGGTAGGCTCATG

E A P A L G Q H E E D L D D Q D V L G A E M R T R  
 kan r

GTGCTCGCTCGATCGGATGTTTCGCTTGGTTCGAATGGGCAGGTAGCCGGAICAAAGCGTATGCAGCCGCCGCA  
 4575  
 CACGAGCGAGCTACGCTACAAAGCGAACCACCAGCTTACCCGTCCATCGGCCCTAGTTCGCATACGTCGGCGGCGGT

A R E I R H K A O H D F P C T A P D L T H L R R M  
 kan r

FIG.31R

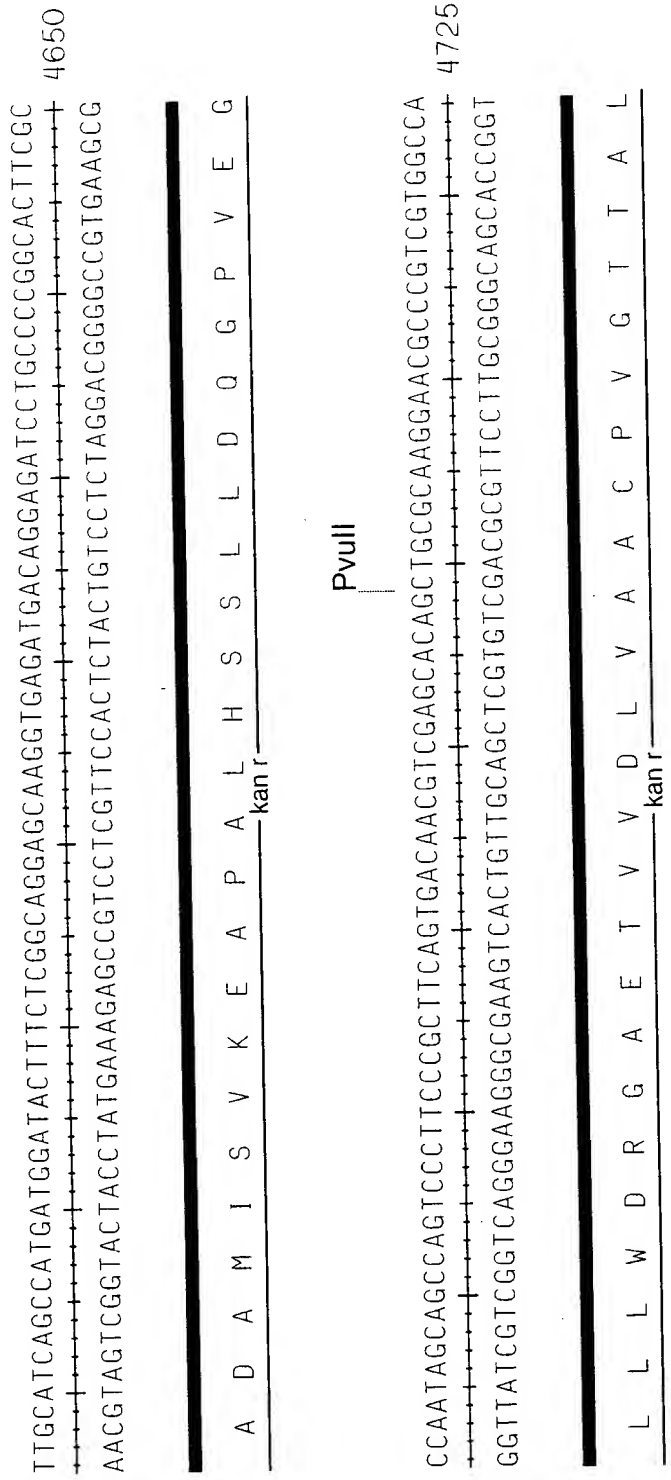


FIG.31S

PstI

GCCACGATAGCCGGCTGCCTCGTCTGCAGTTCAATTCAGGGCACGGACAGGTCGGTCTTGACAAAAAGAACCG  
 4800  
 CGGTGCTATCGGCGGACGGAGCAGGACGTCAAGTAAGTCCCGTGGCTGTCCAGCCAGAACGTGTTTCTTGGC

W S L R A A E D Q L E N L A G S L D T K V F L V P  
 kan r

GCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCGTGTTGTGCCCAGTCATAGCCGA  
 4875  
 CCGCGGGACGGACTGTGCGCCCTTGTCGCCCGGTAGTCTCGTACAGACAACACGGGTGAGTATCGGCT

R G Q A S L R F V A A D S C G I T O O A W D Y G F  
 kan r

ATAGCCTCTCCACCAAGCGGCGGAGAACCTGCGTGCAATCCAATCATTGTTCAATCATGCGAAACGATCCICATC  
 4950  
 TATCGGAGAGGTGGTTCGCCGGCTCTTGGACGCACGTTAGGTAGAACAAGTTAGTACGCTTGTCTAGGAGTAG

L R E V W A A P S G A H L G D O E I M  
 kan r

FIG.31T

BglII

CTGTCTCTTGATCAGATCTTGATCCCCCTGCGCCATCAGATCCTTGGCGGCAAGCAATCCAGTTTACTTTGC  
5025  
GACAGAGAACTAGTCTAGAACTAGGGGACGGGTAGTCTAGGAACCGCCGTTCTTTCCGGTAGGTCAAAATGAAACG

PvuII

AGGGCTTCCCAACCTTACCAGAGGGGCGCCCAAGCTGGCAATTCGGGTTCCGCTTGCTGTCCATAAAACCGCCAGT  
5100  
TCCCGAAGGGTTGGAATGGTCTCCCGGGGGTCGACCGTTAAGGCCAAGCGAACGACAGGTATTTTGGCGGGTCA

CTAGCTATCGCCATGTAGCCCACTGCAAGCTACCTGCTTCTCTTTGCGCTTGCGTTTCCCTTGTCCAGATAG  
5175  
GATCGATAGCGGTACATTCGGGTGACGTTTCGATGGACGAAAGAGAAACGCGAACGCAAAAGGGAACAGGTCTATC

CCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACGCTTCTACGIGTCCGCTTCCCTTAGC  
5250  
GGGTATCGACTGTAAAGTAGGCCCCAGTCGTGGCAAGACGCTGACCGAAAGATGCACAAGGCGAAGGAAATCG

AGCCCTTGGCCCTGAGTGTCTGCGGCAGCGTG  
5283  
TCGGGAACGCGGGACTCACGAACGCGGTGCGAC

FIG.31U